

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 23:13:41 ; Search time 269 Seconds
(without alignments)
12.002 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 38
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358723299 residues

Total number of hits satisfying chosen parameters: 313949

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23sep04:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	94.7	9	2 AAW99195	Aaw99195 Minor his
2	36	94.7	9	2 AAW99196	Aaw99196 Minor his
3	36	94.7	9	2 AAW99197	Aaw99197 Minor his
4	36	94.7	9	2 AAW97572	Aaw97572 T-cell ep
5	36	94.7	9	2 AAW97375	Aaw97375 HA-1 H-a1
6	36	94.7	9	2 AAW97374	Aaw97374 HA-1 R-a1
7	36	94.7	9	8 ADH40333	ADH40333 Human min
8	36	94.7	9	8 ADH40334	ADH40334 Human min
9	23	60.5	9	5 AAU71211	AAU71211 Human MHC
10	23	60.5	9	5 AAU71428	AAU71428 Human MHC
11	22	57.9	9	3 AAY80162	Aay80162 HLA-A2 re
12	22	57.9	9	3 AAU09449	Aau09449 Chlamydia
13	22	57.9	9	6 ABB75298	Abp75298 Chlamydia
14	22	57.9	9	6 ABB75138	Abp75138 Proteome
15	22	57.9	9	6 ABB75181	Abp75181 Proteome
16	21	55.3	6	3 AAB12035	Aab12035 Peptide #
17	21	55.3	6	5 AAU80810	Aau80810 Rat Rb-in
18	21	55.3	6	7 ADE84629	Ade84629 Mammalia
19	21	55.3	8	3 AAB12089	Aab12089 Ad7 cel p
20	21	55.3	8	7 ADE84662	Ade84662 Adenoviru
21	21	55.3	2	2 AAW47427	AAw47427 Prey1 di
22	21	55.3	9	2 AAW97373	AAw97373 Peptide e
23	21	55.3	9	3 AAB12092	Aab12092 Ad40 cel
24	21	55.3	9	3 AAB12086	Aab12086 Cel motif
25	21	55.3	4	4 ABB12506	Abb12506 Human C35

26	21	55.3	9	4 ABB13927	Abb13927 Human C35
27	21	55.3	9	4 ABB12554	Abb12554 Human C35
28	21	55.3	9	4 ABB13072	Abb13072 Human C35
29	21	55.3	9	4 ABB13115	Abb13115 Human C35
30	21	55.3	9	4 ABB13184	Abb13184 Human C35
31	21	55.3	9	4 ABB13867	Abb13867 Human C35
32	21	55.3	9	4 ABB14131	Abb14131 Human C35
33	21	55.3	9	4 ABB12498	Abb12498 Human C35
34	21	55.3	9	4 ABB13144	Abb13144 Human C35
35	21	55.3	9	4 ABB14390	Abb14390 Human C35
36	21	55.3	9	4 ABB14414	Abb14414 Human C35
37	21	55.3	9	4 ABB12651	Abb12651 Human C35
38	21	55.3	9	4 ABB13415	Abb13415 Human C35
39	21	55.3	9	4 ABB13491	Abb13491 Human C35
40	21	55.3	9	4 ABB12658	Abb12658 Human C35
41	21	55.3	9	4 ABB12774	Abb12774 Human C35
42	21	55.3	9	4 ABB12808	Abb12808 Human C35
43	21	55.3	9	4 ABB12983	Abb12983 Human C35
44	21	55.3	9	4 ABB12995	Abb12995 Human C35
45	21	55.3	9	4 ABB13206	Abb13206 Human C35

ALIGNMENTS

RESULT 1					
ID	AAW99195	standard; peptide; 9 AA.			
XX	AAW99195;				
DT	20-MAY-1999	(first entry)			
XX					
DE	Minor histocompatibility antigen HA-1 T-cell epitope #1.				
XX					
KW	Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;				
KW	graft versus host disease; bone marrow transplant; leukaemia; vaccine;				
KW	diagnosis; aplastic anaemia; immune deficiency disease.				
XX					
OS	Homo sapiens.				
XX					
FT	Key	Location/Qualifiers			
FT	Misc-difference 3	/label= His, Arg			
XX					
PN	W09905174-A1.				
XX					
PD	04-FEB-1999.				
XX					
PF	23-JUL-1998; 98WO-NL000425.				
XX					
PR	23-JUL-1997; 97EP-00202303.				
XX					
PA	(UYLE-) RICKSONIV LEIDEN.				
XX					
PI	Goulmy EAJM, Hunt DF, Engelhard VH;				
DR	WPI, 1999-153312/13.				
XX					
PT	A new minor histocompatibility antigen, HA-1 - useful to treat immune				
PT	diseases and prevent rejection and host versus graft disease in bone				
PT	marrow and organ transplantation.				
XX					
PS	Claim 1; Page 32; 47pp; English.				
XX					
CC	The present sequence represents a new peptide (P1) constituting a T-cell				
CC	epitope obtainable from the minor histocompatibility antigen HA-1. The				
CC	peptide is immunogenic and can be used as part of a vaccine. P1 is used				
CC	as a medicine, to induce tolerance for transplants, prevent rejection				
CC	and/or graft versus host disease, or to treat (auto) immune diseases. In				
CC	particular it can be used with bone marrow transplantation, in the				
CC	treatment of severe aplastic anaemia, leukaemia, and immune deficiency				

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CC diseases
XX
SQ Sequence 9 AA;

Query Match      94.7%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
   |||||
Db 1 VLXDDLLEA 9

RESULT 2
AAW99196
ID AAW99196 standard; peptide; 9 AA.
AC AAW99196;
DT 20-MAY-1999 (first entry)
DE Minor histocompatibility antigen HA-1 T-cell epitope #2.
XX
XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KM graft versus host disease; bone marrow transplant; leukaemia; vaccine;
XX diagnosis; aplastic anaemia; immune deficiency disease.
XX Homo sapiens.
XX OS
XX WO9905174-A1.
XX PN
XX PD 04-FEB-1999.
XX PF 23-JUL-1998; 98WO-NL000425.
XX PR 23-JUL-1997; 97EP-00202303.
XX PA (UYLE-) RIJXSUNIV LEIDEN.
XX PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX DR WPI: 1999-15312/13.
XX
XX A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PR marrow and organ transplantation.
XX
XX Claim 3; Page 32; 47pp; English.
XX
XX The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
CC
SQ Sequence 9 AA;

Query Match      94.7%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
   |||||
Db 1 VLHDDLLEA 9

RESULT 3
AAW99197
ID AAW99197 standard; peptide; 9 AA.
XX

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AC AAW99197;
XX
XX 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #3.
XX
XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KM graft versus host disease; bone marrow transplant; leukaemia; vaccine;
XX diagnosis; aplastic anaemia; immune deficiency disease.
XX Homo sapiens.
XX OS
XX WO9905174-A1.
XX PN
XX PD 04-FEB-1999.
XX PF 23-JUL-1998; 98WO-NL000425.
XX PR 23-JUL-1997; 97EP-00202303.
XX PA (UYLE-) RIJXSUNIV LEIDEN.
XX PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX DR WPI: 1999-15312/13.
XX
XX A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PR marrow and organ transplantation.
XX
XX Disclosure; Page 15; 47pp; English.
XX
XX The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
CC
SQ Sequence 9 AA;

Query Match      94.7%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
   |||||
Db 1 VLHDDLLEA 9

RESULT 4
AAW97572
ID AAW97572 standard; peptide; 9 AA.
XX
XX AAW97572;
XX AC
XX
XX 20-MAY-1999 (first entry)
XX
XX T-cell epitope from the minor histocompatibility antigen HA-1.
DE T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
XX T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KM transplant rejection; Graft-versus-Host Disease; autoimmune disease;
XX neoplastic haematopoietic cell.
XX
XX Homo sapiens.
XX OS
XX
XX Key Location/Qualifiers
FH Misc-difference 3 /note= "His or Arg"
FT
XX
XX WO9905173-A1.
XX

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```

XX 04-FEB-1999.
PD
XX
XX 23-JUL-1998; 98WO-NL000424.
PF
XX 23-JUL-1997; 97EP-00202303.
PR
XX (UYLE-) RIKXSUNIV LEIDEN.
PA
XX Goulmy EAJM, Hunt DF, Engelhard VH;
PI
XX WPI; 1999-142855/12.
DR
XX
XX Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT for inducing tolerance to transplants and prevent rejection or graft-
PT versus-host disease.
XX
XX Claim 1; Page 39; 57pp; English.
PS
XX The present sequence represents an immunogenic peptide constituting a T-
CC cell epitope, obtainable from the minor histocompatibility antigen HA-1.
CC The peptide can be used in vaccines or pharmaceutical formulations as
CC medicines to induce tolerance for transplants so as to prevent rejection
CC and/or Graft-versus-Host Disease, or to treat autoimmune diseases.
CC Neoplastic haematopoietic cells presenting the peptides, in an HLA class
CC I context, can be eliminated after specific recognition of the peptides.
CC The peptides can also be used to raise antibodies, T-cell receptor, B-
CC and T-cells
XX
XX Sequence 9 AA;
SQ

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Query Match          94.7%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 VLXDDLLEA 9
   |||||
Db 1 VLXDDLLEA 9

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RESULT 5
AAW97375
ID AAW97375 standard; protein; 9 AA.
XX
XX AAW97375;
AC
XX
XX 13-MAY-1999 (first entry)
DT
XX
XX HA-1 H-allele sequence.
DE
XX
XX Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KM R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KM severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9905313-A2.
PN
XX
XX 04-FEB-1999.
PD
XX
XX 23-JUL-1998; 98WO-EP004928.
PF
XX
XX 23-JUL-1997; 97EP-00202303.
PR
XX 02-JUN-1998; 98EP-00870125.
XX
XX (UYLE-) RIKXSUNIV LEIDEN.
PA
XX
XX Goulmy E;
PI
XX
XX WPI; 1999-142960/12.
DR
XX
XX Typing minor histocompatibility antigen HA-1 - by amplifying and
PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection

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PT of genetic aberrances.
XX
XX Claim 18; Fig 5; 59pp; English.
PS
XX
XX The present sequence represents part of the minor histocompatibility
CC antigen HA-1 H-allele. The specification describes methods for typing
CC alleles (preferably the H and R alleles) of the minor histocompatibility
CC antigen HA-1 in a sample, which comprise detecting polymorphic
CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC methods can be used for HA-1 typing for bone marrow transplants, severe
CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC detection of genetic aberrances. The probes and primers of the invention
CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
XX anti-idiotypic B cells and/or T cells and antibodies
XX
XX Sequence 9 AA;
SQ

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Query Match          94.7%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 VLXDDLLEA 9
   |||||
Db 1 VLXDDLLEA 9

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RESULT 6
AAW97374
ID AAW97374 standard; protein; 9 AA.
XX
XX AAW97374;
AC
XX
XX 13-MAY-1999 (first entry)
DT
XX
XX HA-1 R-allele sequence.
DE
XX
XX Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KM R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KM severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9905313-A2.
PN
XX
XX 04-FEB-1999.
PD
XX
XX 23-JUL-1998; 98WO-EP004928.
PF
XX
XX 23-JUL-1997; 97EP-00202303.
PR
XX 02-JUN-1998; 98EP-00870125.
XX
XX (UYLE-) RIKXSUNIV LEIDEN.
PA
XX
XX Goulmy E;
PI
XX
XX WPI; 1999-142960/12.
DR
XX
XX Typing minor histocompatibility antigen HA-1 - by amplifying and
PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT of genetic aberrances.
XX
XX Claim 13; Fig 5; 59pp; English.
PS
XX
XX The present sequence represents part of the minor histocompatibility
CC antigen HA-1 R-allele. The specification describes methods for typing
CC alleles (preferably the H and R alleles) of the minor histocompatibility
CC antigen HA-1 in a sample, which comprise detecting polymorphic
CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC methods can be used for HA-1 typing for bone marrow transplants, severe
CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC detection of genetic aberrances. The probes and primers of the invention
CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
CC anti-idiotypic B cells and/or T cells and antibodies

```


AC AAU71211;
XX 26-FEB-2002 (first entry)
XX
XX Human MHC class I molecule HLA-A2 binding 103P3E8 peptide #18.
DE
XX 103P3E8; prostate; bladder; kidney; colon; lung; breast; rectum; stomach;
KW tumor; cancer; cytostatic; gene therapy; antibody therapy; ribozyme;
KW single chain monoclonal antibody; serum; blood; urine; tissue; human;
KW chromosome 9q13-q21.
XX
OS Homo sapiens.
XX
XX WO200179557-A2.
XX
XX 25-OCT-2001.
XX
XX 12-APR-2001; 2001WO-US012181.
XX
XX 12-APR-2000; 2000US-0196647P.
XX
XX (UROC-) UROGENESYS INC.
XX
XX Paris M, Chailita-Bid PM, Raitano AB, Mitchell SC, Afar DEH;
PI Jakovcits A;
XX
XX WPI; 2002-061976/08.
XX
XX Monitoring 103P3E8 gene products in sample from patient (suspected of)
PT having cancer, useful for diagnosing, managing or treating cancers, e.g.
PT prostate cancer, comprises determining presence of aberrant 103P3E8 gene
PT products.
XX
XX
XX Disclosure; Page 84; 128pp; English.
XX
XX Sequences AAU71093-AAU71796 represent the 103P3E8-related protein and
CC peptide fragments of the protein. 103P3E8 exhibits tissue specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumors of the prostate, bladder, kidney, colon,
CC lung, breast, rectum and stomach. The 103P3E8 polynucleotide, its related
CC protein and peptide fragments and specific PCR primers are therefore
CC useful for diagnosing and treating cancer. A vector comprising a
CC polynucleotide which encodes a single chain monoclonal antibody, that
CC immunospecifically binds to an 103P3E8-related protein, and a ribozyme
CC capable of cleaving a polynucleotide having the 103P3E8 coding sequence,
CC are both useful in the preparation of a composition for treating a
CC patient with a cancer that expresses 103P3E8. The sequences can be used
CC in diagnostic methods to monitor the level of 103P3E8 gene products in
CC serum, blood, urine and tissue and to thereby detect the presence of
CC cancerous cells
XX
XX
SQ Sequence 9 AA;

Query Match 60.5%; Score 23; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLEA 9
DB 1 DLEA 5

RESULT 10
AAU71428
ID AAU71428 standard; peptide; 9 AA.
XX
XX AAU71428;
AC
XX
XX 26-FEB-2002 (first entry)
DT
XX
XX Human MHC molecule HLA-A11 binding 103P3E8 peptide #35.
DE
XX
XX 103P3E8; prostate; bladder; kidney; colon; lung; breast; rectum; stomach;

KW tumor; cancer; cytostatic; gene therapy; antibody therapy; ribozyme;
KW single chain monoclonal antibody; serum; blood; urine; tissue; human;
KW chromosome 9q13-q21.
XX
XX Homo sapiens.
XX
XX WO200179557-A2.
XX
XX 25-OCT-2001.
XX
XX 12-APR-2001; 2001WO-US012181.
XX
XX 12-APR-2000; 2000US-0196647P.
XX
XX (UROC-) UROGENESYS INC.
XX
XX Paris M, Chailita-Bid PM, Raitano AB, Mitchell SC, Afar DEH;
PI Jakovcits A;
XX
XX WPI; 2002-061976/08.
XX
XX Monitoring 103P3E8 gene products in sample from patient (suspected of)
PT having cancer, useful for diagnosing, managing or treating cancers, e.g.
PT prostate cancer, comprises determining presence of aberrant 103P3E8 gene
PT products.
XX
XX
XX Disclosure; Page 90; 128pp; English.
XX
XX Sequences AAU71093-AAU71796 represent the 103P3E8-related protein and
CC peptide fragments of the protein. 103P3E8 exhibits tissue specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumors of the prostate, bladder, kidney, colon,
CC lung, breast, rectum and stomach. The 103P3E8 polynucleotide, its related
CC protein and peptide fragments and specific PCR primers are therefore
CC useful for diagnosing and treating cancer. A vector comprising a
CC polynucleotide which encodes a single chain monoclonal antibody, that
CC immunospecifically binds to an 103P3E8-related protein, and a ribozyme
CC capable of cleaving a polynucleotide having the 103P3E8 coding sequence,
CC are both useful in the preparation of a composition for treating a
CC patient with a cancer that expresses 103P3E8. The sequences can be used
CC in diagnostic methods to monitor the level of 103P3E8 gene products in
CC serum, blood, urine and tissue and to thereby detect the presence of
CC cancerous cells
XX
XX
SQ Sequence 9 AA;

Query Match 60.5%; Score 23; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLEA 9
DB 5 DLEA 9

RESULT 11
AAV80162
ID AAV80162 standard; peptide; 9 AA.
XX
XX AAV80162;
AC
XX
XX 24-MAY-2000 (first entry)
DT
XX
XX HLA-A2 restricted tumour antigen peptide derived from SART-1 #15.
DE
XX
XX HLA-A2 restricted tumour antigen; SART-1; human leukocyte antigen; human;
KW diagnosis; tumour; cytotoxic T cell; flat epithelioma; lung cancer;
KW oesophagus cancer; cytostatic.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX WO200006595-A1.

XX 10-FEB-2000.
 XX 27-JUL-1999; 99WO-JP004010.
 XX 28-JUL-1998; 98JP-00212940.
 XX (SUMU) SUMITOMO PHARM CO LTD.
 XX (ITOH/) ITOH K.
 XX Itoh K, Kobayashi T;
 XX WPI, 2000-195258/17.
 XX HLA-A2 resistant tumor antigen peptides derived from SART-1, useful as
 XX preventives or diagnostics for tumors e.g. flat epithelioma like lung
 XX cancer.
 XX Claim 2, Page 41, 55pp; Japanese.
 XX AAY80148 to AAY80181 represent specifically claimed HLA-A2 restricted
 XX tumour antigen peptides derived from SART-1. The peptides have cytostatic
 XX activity. The peptides are useful as a preventive or diagnostic for
 XX tumours e.g. flat epithelioma like lung cancer and oesophagus cancer
 XX Sequence 9 AA;
 SQ

Query Match 57.9%; Score 22; DB 3; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2;

OY 1 VLXDDL 7
 Db 3 VRADDL 9

RESULT 12
 AAU09449
 ID AAU09449 standard; peptide; 9 AA.
 AC AAU09449;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Chlamydia pneumoniae T-cell epitope #4 useful as Chlamydia antigen.
 XX
 KM ATP binding cassette; secretory locus open reading frame; endopeptidase;
 KM secretory locus ORF; protease; metalloprotease; CLP protease ATPase;
 KM CLP protease subunit; transglycolase/transpeptidase; CLPC protease;
 KM thioredoxin; Chlamydia infection; antibacterial; immunogen.
 XX
 OS Chlamydia pneumoniae CML029.
 XX
 PN WO200185972-A2.
 PD 15-NOV-2001.
 XX
 PF 08-MAY-2001; 2001WO-CA000653.
 XX
 PR 08-MAY-2000; 2000US-0202672P.
 PR 30-MAY-2000; 2000US-0207852P.
 PR 16-JUN-2000; 2000US-0211796P.
 PR 16-JUN-2000; 2000US-0211797P.
 PR 16-JUN-2000; 2000US-0211798P.
 PR 16-JUN-2000; 2000US-0211801P.
 PR 16-JUN-2000; 2000US-0212044P.
 PR 26-SEP-2000; 2000US-0235335P.
 PR 26-SEP-2000; 2000US-0235361P.
 PR 26-SEP-2000; 2000US-0235398P.
 XX
 PA (AVERT) AVENTIS PASTEUR LTD.
 XX
 PI Murdin AD, Oomen RP, Wang J, Dunn P;

XX WPI, 2002-049447/06.
 XX Vaccine useful for immunizing mammals against chlamydia infections,
 XX comprises vectors having sequences of ATP binding cassette gene,
 XX secretory locus open reading frame gene of chlamydia.
 XX Example 4; Page 80; 355pp; English.

XX The present invention relates to the isolation of Chlamydia pneumoniae
 XX pneumoniae strain CML029 genes and their encoded proteins. The genes of
 XX the invention encode an ATP binding cassette gene, a secretory locus open
 XX reading frame (ORF), an endopeptidase, a protease, a metalloprotease, CLP
 XX protease ATPase, a CLP protease subunit, a transglycolase/transpeptidase,
 XX a CLPC protease, or thioredoxin. The genes of the invention can be used
 XX in a vector as a vaccine for the prevention and treatment of Chlamydia
 XX infections. AAU09440-AAU09473 represent B- or T-cell epitopes from the C.
 XX pneumoniae proteins (AAU09430-AAU09439) of the invention. These epitopes
 XX can be used as Chlamydia antigens
 XX Sequence 9 AA;
 SQ

Query Match 57.9%; Score 22; DB 5; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
 Matches 4; Conservative 2; Mismatches 1;

OY 2 LXDDE 8
 Db 2 LGDELE 8

RESULT 13
 ABP75298
 ID ABP75298 standard; peptide; 9 AA.
 AC ABP75298;
 XX
 DT 20-FEB-2003 (first entry)
 XX
 DE Chlamydia pneumoniae peptide epitope #64.
 XX
 KM Antibacterial; secreted protein; intracellular bacterium.
 XX
 OS Chlamydia pneumoniae.
 XX
 PN WO200282091-A2.
 PD 17-OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-DK000234.
 XX
 PR 09-APR-2001; 2001DK-00000581.
 PR 09-APR-2001; 2001US-0282513P.
 XX
 PA (SHAW/) SHAW A C.
 PA (VAND/) VANDAH B B.
 XX
 PI Shaw AC, Vandahl BB;
 XX
 DR WPI, 2003-058585/05.
 XX
 PR Identifying intracellular bacterial proteins by labeling proteins in the
 XX presence of a eukaryotic protein synthesis inhibitor, performing
 XX electrophoresis, autoradiography and comparing profiles to an infected-
 XX cell lysate profile.
 XX Claim 34; Page 151, 179pp; English.
 XX
 CC The present invention relates to a method (M1) for identifying secreted
 XX intracellular bacterial proteins (BP). M1 comprises: (a) selectively
 XX visualising BP by pulse labelling in the presence of an inhibitor of
 XX eukaryotic protein synthesis followed by 2D electrophoresis and
 XX autoradiography; (b) comparing protein profiles (PP) of purified bacteria

CC to PF of total lysate (TL) of infected cells; and (c) identifying protein
CC spots present in differential images from gels loaded with TL. The
CC present sequence is one such bacterial peptide epitope which was
CC identified by the method of the invention

XX Sequence 9 AA;

Query Match 57.9%; Score 22; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 LXDLDLE 8
| | | | |
Db 2 LGDLE 8

RESULT 14
ABP75138
ID ABP75138 standard; peptide; 9 AA.

XX ABP75138;

DT 03-FEB-2003 (first entry)

DE Proteome analysis related peptide #423.

XX Proteome analysis; isolation; determination; diagnostic assay; detection;
KM protein marker; identification; metastatic; invasive cancer;
XX differential expression; signalling pathway; chromatography.

OS Synthetic.

PN WO200277016-A2.

PD 03-OCT-2002.

PF 22-MAR-2002; 2002WO-EP003368.

PR 22-MAR-2001; 2001US-0278171P.

PR 12-SEP-2001; 2001US-0318749P.

PR 20-SEP-2001; 2001US-0323999P.

XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

XX Vandekerckhove J, Gevaert K;

DR WPI; 2003-067379/06.

PT Method for isolation of peptides from complex mixture of peptides
PT involves specific chemical and/or enzymatic alteration of at least one
PT type of peptide.

PS Example 22; Page 150; 193pp; English.

XX The present invention describes a method (M1) for the isolation of a
CC subset of peptides from a protein peptide mixture (P1). M1 involves: (a)
CC separating the protein peptide mixture into fractions of peptides via
CC chromatography; (b) chemically, or enzymatically, or chemically and
CC enzymatically, altering at least one amino acid of at least one of the
CC peptides in each fraction, thereby generating a subset of altered
CC peptides; and (c) isolating the altered (flagged) peptides out of each
CC fraction via chromatography, where the chromatography of steps (a) and
CC (c) is performed with the same type of chromatography. M1 can be used for
CC the isolation and determination of peptides from protein peptide
CC mixtures. M1 can also be used in diagnostic assays for detection of the
CC presence, the absence or a variation in expression level of at least one
CC protein marker or a specific set of proteins indicative of a disease
CC state. M1 can be used for identifying target proteins present in
CC metastatic and invasive cancers, in differential expression of proteins
CC in transgenic mice, identification of proteins that are upregulated or
CC down regulated in disease tissues, in identification of intracellular
CC changes in cells with physiological changes such as metabolic shift, in
CC the identification of biomarkers in cancers and in the identification of

CC signalling pathways. The method is gel-free methodology for qualitative
CC and quantitative proteome analysis without the need for multidimensional
CC chromatography and without the use of affinity tags. ABP74714 to ABP75190
CC represent peptide sequences used in the exemplification of the present
CC invention

XX Sequence 9 AA;

Query Match 57.9%; Score 22; DB 6; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 LXDLDLE 8
| | | | |
Db 3 LLDLSE 9

RESULT 15
ABP75181
ID ABP75181 standard; peptide; 9 AA.

XX ABP75181;

DT 03-FEB-2003 (first entry)

DE Proteome analysis related peptide #466.

XX Proteome analysis; isolation; determination; diagnostic assay; detection;
KM protein marker; identification; metastatic; invasive cancer;
XX differential expression; signalling pathway; chromatography.

OS Synthetic.

PN WO200277016-A2.

PD 03-OCT-2002.

PF 22-MAR-2002; 2002WO-EP003368.

PR 22-MAR-2001; 2001US-0278171P.

PR 12-SEP-2001; 2001US-0318749P.

PR 20-SEP-2001; 2001US-0323999P.

XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

XX Vandekerckhove J, Gevaert K;

DR WPI; 2003-067379/06.

PT Method for isolation of peptides from complex mixture of peptides
PT involves specific chemical and/or enzymatic alteration of at least one
PT type of peptide.

PS Example 22; Page 151; 193pp; English.

XX The present invention describes a method (M1) for the isolation of a
CC subset of peptides from a protein peptide mixture (P1). M1 involves: (a)
CC separating the protein peptide mixture into fractions of peptides via
CC chromatography; (b) chemically, or enzymatically, or chemically and
CC enzymatically, altering at least one amino acid of at least one of the
CC peptides in each fraction, thereby generating a subset of altered
CC peptides; and (c) isolating the altered (flagged) peptides out of each
CC fraction via chromatography, where the chromatography of steps (a) and
CC (c) is performed with the same type of chromatography. M1 can be used for
CC the isolation and determination of peptides from protein peptide
CC mixtures. M1 can also be used in diagnostic assays for detection of the
CC presence, the absence or a variation in expression level of at least one
CC protein marker or a specific set of proteins indicative of a disease
CC state. M1 can be used for identifying target proteins present in
CC metastatic and invasive cancers, in differential expression of proteins
CC in transgenic mice, identification of proteins that are upregulated or
CC down regulated in disease tissues, in identification of intracellular
CC changes in cells with physiological changes such as metabolic shift, in

CC the identification of biomarkers in cancers and in the identification of
CC signalling pathways. The method is gel-free methodology for qualitative
CC and quantitative proteome analysis without the need for multidimensional
CC chromatography and without the use of affinity tags. ABP74714 to ABP75190
CC represent peptide sequences used in the exemplification of the present
CC invention

XX
SQ Sequence 9 AA;

Query Match 57.9%; Score 22; DB 6; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LKDDLL 8
| | | | |
| | | | |
Db 3 LKDDLSB 9

Search completed: December 29, 2004, 23:29:52
Job time : 274 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 23:24:55 ; Search time 37 Seconds

(without alignments)
16.131 Million cell updates/sec

Title: US-10-791-217A-1

Perfect score: 38

Sequence: 1 VLXDDLERA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 95011

Minimum DB seq length: 0
Maximum DB seq length: 95

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:*

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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	57.9	7	US-08-556-419-14	Sequence 14, Appl
2	22	57.9	9	US-09-744-549-15	Sequence 15, Appl
3	21	55.3	6	US-08-459-568-20	Sequence 20, Appl
4	21	55.3	6	US-08-399-411-20	Sequence 20, Appl
5	21	55.3	6	US-08-516-859A-20	Sequence 20, Appl
6	21	55.3	6	US-09-586-472-20	Sequence 20, Appl
7	21	55.3	6	US-09-528-706-20	Sequence 20, Appl
8	21	55.3	6	US-08-459-568-75	Sequence 20, Appl
9	21	55.3	8	US-08-399-411-75	Sequence 20, Appl
10	21	55.3	8	US-08-516-859A-75	Sequence 20, Appl
11	21	55.3	8	US-09-586-472-75	Sequence 20, Appl
12	21	55.3	8	US-09-528-706-75	Sequence 20, Appl
13	21	55.3	9	US-08-459-568-72	Sequence 20, Appl
14	21	55.3	9	US-08-459-568-78	Sequence 20, Appl
15	21	55.3	9	US-08-399-411-72	Sequence 20, Appl
16	21	55.3	9	US-08-516-859A-72	Sequence 20, Appl
17	21	55.3	9	US-08-399-411-78	Sequence 20, Appl
18	21	55.3	9	US-08-516-859A-78	Sequence 20, Appl
19	21	55.3	9	US-09-528-706-78	Sequence 20, Appl
20	21	55.3	9	US-08-459-568-11	Sequence 20, Appl
21	21	55.3	9	US-08-873-235B-11	Sequence 20, Appl
22	21	55.3	9	US-09-586-472-72	Sequence 20, Appl
23	21	55.3	9	US-09-586-472-78	Sequence 20, Appl
24	21	55.3	9	US-09-528-706-72	Sequence 20, Appl
25	21	55.3	9	US-09-528-706-78	Sequence 20, Appl
26	20	52.6	6	US-09-023-819-11	Sequence 11, Appl
27	20	52.6	6	US-09-808-126-11	Sequence 11, Appl
28	20	52.6	6	US-09-803-951-11	Sequence 11, Appl

28	20	52.6	8	US-08-747-539A-47	Sequence 47, Appl
29	20	52.6	8	US-08-747-539A-50	Sequence 50, Appl
30	20	52.6	8	US-08-747-539A-51	Sequence 51, Appl
31	19	50.0	6	US-08-974-549A-373	Sequence 373, Appl
32	19	50.0	6	US-08-912-951-140	Sequence 140, Appl
33	19	50.0	6	US-09-402-161B-373	Sequence 373, Appl
34	19	50.0	7	US-09-721-456-373	Sequence 373, Appl
35	19	50.0	7	US-09-187-859-1186	Sequence 1186, Appl
36	19	50.0	7	US-09-839-542B-1186	Sequence 1186, Appl
37	19	50.0	8	US-09-187-859-1189	Sequence 1189, Appl
38	19	50.0	8	US-09-187-859-2550	Sequence 2550, Appl
39	19	50.0	8	US-09-183-266A-35	Sequence 35, Appl
40	19	50.0	8	US-09-183-266A-36	Sequence 36, Appl
41	19	50.0	8	US-09-183-266A-38	Sequence 38, Appl
42	19	50.0	8	US-09-839-542B-1189	Sequence 1189, Appl
43	19	50.0	8	US-09-839-542B-2550	Sequence 2550, Appl
44	19	50.0	9	US-07-663-413-15	Sequence 15, Appl
45	19	50.0	9	US-08-055-530-15	Sequence 15, Appl

ALIGNMENTS

```
RESULT 1
US-08-556-419-14
; Sequence 14, Application US/08556419C
; Patent No. 6093549
; GENERAL INFORMATION:
; APPLICANT: Ross, Christopher
; APPLICANT: Li, Xiao-Jiang
; APPLICANT: Li, Shi-Hua
; APPLICANT: Sharp, Alan
; APPLICANT: Lananhan, Anthony
; APPLICANT: Morley, Paul
; APPLICANT: Snyder, Solomon
; TITLE OF INVENTION: Huntingtin-associated protein
; FILE REFERENCE: 01107.52271
; CURRENT APPLICATION NUMBER: US/08/556,419C
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-08-556-419-14

Query Match      57.9%   Score 22;   DB 3;   Length 7;
Best Local Similarity 80.0%   Pred. No. 3.8e+05;
Matches 4;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

QY      4 DDLLE 8
      ||||:
Db      1 DDLQ 5

RESULT 2
US-09-744-549-15
; Sequence 15, Application US/09744549
; Patent No. 6664232
; GENERAL INFORMATION:
; APPLICANT: Itoh, Kyogo et al.
; TITLE OF INVENTION: HLA-A2-restricted Tumor Antigen Peptides Derived From SART-1
; FILE REFERENCE: 0020-4808P
; CURRENT APPLICATION NUMBER: US/09/744,549
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: JP H10-212940
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
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ORGANISM: Homo sapiens
US-09-744-549-15

Query Match 57.9%; Score 22; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0;

QY 1 VLXDDL 7
| | | | |
Db 3 VRADDL 9

RESULT 3

US-08-459-568-20
Sequence 20, Application US/08459568
Patent No. 581304

GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,568
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-459-568-20

Query Match 55.3%; Score 21; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
: | | | |
Db 1 EDLLE 5

RESULT 4

US-08-399-411-20
Sequence 20, Application US/08399411
Patent No. 5831008

GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-399-411-20

Query Match 55.3%; Score 21; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
: | | | |
Db 1 EDLLE 5

RESULT 5

US-08-516-859A-20
Sequence 20, Application US/08516859A
Patent No. 6069231

GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516,859A
FILING DATE: 18-AUG-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-516-859A-20

Query Match 55.3%; Score 21; DB 3; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
DB 1 EDLE 5

RESULT 6
US-09-586-472-20
Sequence 20, Application US/09586472
Patent No. 6323335
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-586-472-20

Query Match 55.3%; Score 21; DB 3; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8

DB 1 EDLE 5

RESULT 7
US-09-528-706-20
Sequence 20, Application US/09528706
Patent No. 6468985
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,706
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/516,859
FILING DATE:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-09-528-706-20

Query Match 55.3%; Score 21; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
DB 1 EDLE 5

RESULT 8
US-08-459-568-75
Sequence 75, Application US/08459568
Patent No. 5811304
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,568
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-459-568-75

Query Match 55.3%; Score 21; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLLE 8
:||||
Db 1 EDLLE 5

RESULT 9
US-08-399-411-75
Sequence 75, Application US/08399411
Patent No. 5831008
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-399-411-75
Query Match 55.3%; Score 21; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLLE 8
:||||
Db 1 EDLLE 5

RESULT 10
US-08-516-859A-75
Sequence 75, Application US/08516859A
Patent No. 6069231
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516,859A
FILING DATE: 18-AUG-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-516-859A-75

Query Match 55.3%; Score 21; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLLE 8
:||||
Db 1 EDLLE 5

RESULT 11
US-09-586-472-75
Sequence 75, Application US/09586472
Patent No. 6323335
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
Zinc Finger Proteins

NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-586-472-75

Query Match 55.3%; Score 21; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
:||||
Db 1 EDLLE 5

RESULT 12
US-09-528-706-75
Sequence 75, Application US/09528706
Patent No. 6468985
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,706

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/516,859
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-528-706-75

Query Match 55.3%; Score 21; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLE 8
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Db 1 EDLLE 5

RESULT 13
US-08-459-568-72
Sequence 72, Application US/08459568
Patent No. 5811304
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,568
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-459-568-72

Query Match 55.3%; Score 21; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLLE 8
:||||
Db 1 EDLLE 5

RESULT 14

US-08-459-568-78
; Sequence 78, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,568
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-459-568-78

Query Match 55.3%; Score 21; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLLE 8
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Db 1 EDLLE 5

RESULT 15
US-08-399-411-72
; Sequence 72, Application US/08399411
; Patent No. 5831008
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego

; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,411
; FILING DATE: 06-MAR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-399-411-72

Query Match 55.3%; Score 21; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLLE 8
:||||
Db 1 EDLLE 5

Search completed: December 29, 2004, 23:34:37
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 23:33:19 ; Search time 159 Seconds
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20.362 Million cell updates/sec

Title: US-10-791-217a-1
Perfect score: 38
Sequence: 1 VLXDDLEA 9

Scoring table: BLOSUM62
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Searched: 1599051 seqs, 35972711 residues

Total number of hits satisfying chosen parameters: 139774

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	36	94.7	9	US-10-623-176-1	Sequence 1, Appl1
2	36	94.7	9	US-10-623-176-2	Sequence 2, Appl1
3	36	94.7	9	US-10-623-176-10	Sequence 10, Appl1
4	36	94.7	9	US-10-791-217-1	Sequence 1, Appl1
5	36	94.7	9	US-10-791-217-2	Sequence 2, Appl1
6	36	94.7	9	US-10-791-217-5	Sequence 5, Appl1
7	32	84.2	9	US-10-623-176-41	Sequence 41, Appl1
8	32	84.2	9	US-10-623-176-42	Sequence 42, Appl1
9	32	84.2	9	US-10-623-176-45	Sequence 45, Appl1
10	32	84.2	9	US-10-623-176-46	Sequence 46, Appl1
11	29	76.3	9	US-10-623-176-47	Sequence 47, Appl1
12	29	76.3	9	US-10-623-176-48	Sequence 48, Appl1
13	27	71.1	9	US-10-623-176-23	Sequence 23, Appl1

14	27	71.1	9	US-10-623-176-40	Sequence 40, Appl1
15	23	60.5	8	US-10-623-176-15	Sequence 15, Appl1
16	23	60.5	9	US-09-834-765-132	Sequence 132, App
17	23	60.5	9	US-09-834-765-349	Sequence 349, App
18	23	60.5	9	US-10-623-176-3	Sequence 3, Appl1
19	23	60.5	9	US-10-623-176-4	Sequence 4, Appl1
20	23	60.5	9	US-10-623-176-5	Sequence 5, Appl1
21	22	57.9	9	US-10-119-536A-109	Sequence 109, App
22	22	57.9	9	US-10-394-980-421	Sequence 421, App
23	22	57.9	9	US-10-394-980-464	Sequence 464, App
24	22	57.9	9	US-10-275-652-50	Sequence 50, Appl1
25	21	55.3	9	US-09-833-203-54	Sequence 54, Appl1
26	21	55.3	9	US-10-057-475B-10608	Sequence 10608, A
27	21	55.3	9	US-10-057-475B-10813	Sequence 10813, A
28	21	55.3	9	US-10-154-884B-10608	Sequence 10608, A
29	21	55.3	9	US-10-154-884B-10813	Sequence 10813, A
30	21	55.3	9	US-10-623-176-14	Sequence 14, Appl1
31	21	55.3	9	US-10-791-217-4	Sequence 4, Appl1
32	21	55.3	9	US-10-809-790-23	Sequence 23, Appl1
33	20	52.6	5	US-10-166-225A-168	Sequence 168, App
34	20	52.6	5	US-10-166-225A-169	Sequence 169, App
35	20	52.6	5	US-10-166-225A-170	Sequence 170, App
36	20	52.6	5	US-10-166-225A-171	Sequence 171, App
37	20	52.6	5	US-10-166-225A-172	Sequence 172, App
38	20	52.6	5	US-10-166-225A-173	Sequence 173, App
39	20	52.6	6	US-09-803-951-11	Sequence 11, Appl1
40	20	52.6	6	US-09-803-951-11	Sequence 11, Appl1
41	20	52.6	7	US-10-271-708-8	Sequence 8, Appl1
42	20	52.6	8	US-09-801-784-19	Sequence 19, Appl1
43	20	52.6	8	US-09-801-784-20	Sequence 20, Appl1
44	20	52.6	8	US-09-801-784-21	Sequence 21, Appl1
45	20	52.6	8	US-09-801-784-22	Sequence 22, Appl1

ALIGNMENTS

RESULT 1
US-10-623-176-1
Sequence 1, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Els A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhardt, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT FILING DATE: 2003-07-18
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
OTHER INFORMATION: wherein X can be R or H
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-1
Query Match 94.7%; Score 36; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLXDDLLEA 9
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Db 1 VLXDDLLEA 9

RESULT 2
US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-2

Query Match          94.7%; Score 36; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.5e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VLXDDLLEA 9
   |||||
Db 1 VLXDDLLEA 9

RESULT 3
US-10-623-176-10
; Sequence 10, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-10

Query Match          94.7%; Score 36; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.5e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VLXDDLLEA 9
   |||||
Db 1 VLXDDLLEA 9

RESULT 4
US-10-791-217-1
; Sequence 1, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Engelhard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/10/791,217
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: obtained from histocompatibility antigen
; NAME/KEY: MISC FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is HISTIDINE OR ARGININE RESIDUE
US-10-791-217-1

Query Match          94.7%; Score 36; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLXDDLLEA 9
   |||||
Db 1 VLXDDLLEA 9

RESULT 5
US-10-791-217-2
; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Engelhard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/10/791,217
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
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; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: obtained from histocompatibility antigen
 US-10-791-217-2

Query Match 94.7%; Score 36; DB 17; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.5e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
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 Db 1 VLHDDLLEA 9

RESULT 6
 US-10-791-217-5
 ; Sequence 5, Application US/10791217
 ; Publication No. US20040191268A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goulimy, Elsa A.J.M.
 ; APPLICANT: Hunt, Donald F.
 ; APPLICANT: Engelhard, Victor H.
 ; TITLE OF INVENTION: The HA-1 Antigen
 ; FILE REFERENCE: 2183-4285US
 ; CURRENT APPLICATION NUMBER: US/10/791,217
 ; CURRENT FILING DATE: 2004-03-02
 ; PRIOR APPLICATION NUMBER: US/09/489,760
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: PCT/NL98/00424
 ; PRIOR FILING DATE: 1998-07-23
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: obtained from KIAA0223 partial complementary DNA
 US-10-791-217-5

Query Match 94.7%; Score 36; DB 17; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.5e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
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 Db 1 VLHDDLLEA 9

RESULT 7
 US-10-623-176-41
 ; Sequence 41, Application US/10623176
 ; Publication No. US20040092446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goulimy, Els A.J.M.
 ; APPLICANT: Hunt, Donald F.
 ; APPLICANT: Engelhard, Victor H.
 ; TITLE OF INVENTION: HA-1 epitopes and uses thereof
 ; FILE REFERENCE: 2183-6047US
 ; CURRENT APPLICATION NUMBER: US/10/623,176
 ; CURRENT FILING DATE: 2003-07-18
 ; PRIOR APPLICATION NUMBER: 09/489,760
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: EP 97202303.0
 ; PRIOR FILING DATE: 1997-07-23
 ; PRIOR APPLICATION NUMBER: PCT/NL98/00424
 ; PRIOR FILING DATE: 1998-07-23
 ; PRIOR APPLICATION NUMBER: JP 2000-504165

; PRIOR FILING DATE: 2000-01-24
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 ; SOFTWARE: PatentIn Ver. 2.1
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 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
 ; NAME/KEY: SITE
 ; LOCATION: (1)..(9)
 US-10-623-176-41

Query Match 84.2%; Score 32; DB 15; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.5e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLE 8
 |||||
 Db 2 VLHDDLLE 9

RESULT 8
 US-10-623-176-42
 ; Sequence 42, Application US/10623176
 ; Publication No. US20040092446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goulimy, Els A.J.M.
 ; APPLICANT: Hunt, Donald F.
 ; APPLICANT: Engelhard, Victor H.
 ; TITLE OF INVENTION: HA-1 epitopes and uses thereof
 ; FILE REFERENCE: 2183-6047US
 ; CURRENT APPLICATION NUMBER: US/10/623,176
 ; CURRENT FILING DATE: 2003-07-18
 ; PRIOR APPLICATION NUMBER: 09/489,760
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: EP 97202303.0
 ; PRIOR FILING DATE: 1997-07-23
 ; PRIOR APPLICATION NUMBER: PCT/NL98/00424
 ; PRIOR FILING DATE: 1998-07-23
 ; PRIOR APPLICATION NUMBER: JP 2000-504165
 ; PRIOR FILING DATE: 2000-01-24
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 42
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
 ; NAME/KEY: SITE
 ; LOCATION: (1)..(9)
 US-10-623-176-42

Query Match 84.2%; Score 32; DB 15; Length 9;
 Best Local Similarity 87.5%; Pred. No. 1.5e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLE 8
 |||||
 Db 2 VLHDDLLE 9

RESULT 9
 US-10-623-176-45
 ; Sequence 45, Application US/10623176
 ; Publication No. US20040092446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goulimy, Els A.J.M.
 ; APPLICANT: Hunt, Donald F.
 ; APPLICANT: Engelhard, Victor H.

```
/ TITLE OF INVENTION: HA-1 epitopes and uses thereof
/ FILE REFERENCE: 2183-6047US
/ CURRENT APPLICATION NUMBER: US/10/623,176
/ CURRENT FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/489,760
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: EP 97202303.0
/ PRIOR FILING DATE: 1997-07-23
/ PRIOR APPLICATION NUMBER: PCT/NL98/00424
/ PRIOR FILING DATE: 1998-07-23
/ PRIOR APPLICATION NUMBER: JP 2000-504165
/ PRIOR FILING DATE: 2000-01-24
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 45
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (1)..(9)
US-10-623-176-45
```

```
Query Match      84.2%; Score 32; DB 15; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.5e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 LXDLEA 9
        | | | | |
Db      1 LRDLEA 8
```

```
RESULT 10
US-10-623-176-46
/ Sequence 46, Application US/10623176
/ Publication No. US20040092446A1
/ GENERAL INFORMATION:
/ APPLICANT: Goulmy, Els A.J.M.
/ APPLICANT: Hunt, Donald F.
/ APPLICANT: Engelhard, Victor H.
/ TITLE OF INVENTION: HA-1 epitopes and uses thereof
/ FILE REFERENCE: 2183-6047US
/ CURRENT APPLICATION NUMBER: US/10/623,176
/ CURRENT FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/489,760
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: EP 97202303.0
/ PRIOR FILING DATE: 1997-07-23
/ PRIOR APPLICATION NUMBER: PCT/NL98/00424
/ PRIOR FILING DATE: 1998-07-23
/ PRIOR APPLICATION NUMBER: JP 2000-504165
/ PRIOR FILING DATE: 2000-01-24
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 46
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (1)..(9)
US-10-623-176-46
```

```
Query Match      84.2%; Score 32; DB 15; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.5e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 LXDLEA 9
        | | | | |
```

```
Db      1 LRDLEA 8
```

```
RESULT 11
US-10-623-176-47
/ Sequence 47, Application US/10623176
/ Publication No. US20040092446A1
/ GENERAL INFORMATION:
/ APPLICANT: Goulmy, Els A.J.M.
/ APPLICANT: Hunt, Donald F.
/ APPLICANT: Engelhard, Victor H.
/ TITLE OF INVENTION: HA-1 epitopes and uses thereof
/ FILE REFERENCE: 2183-6047US
/ CURRENT APPLICATION NUMBER: US/10/623,176
/ CURRENT FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/489,760
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: EP 97202303.0
/ PRIOR FILING DATE: 1997-07-23
/ PRIOR APPLICATION NUMBER: PCT/NL98/00424
/ PRIOR FILING DATE: 1998-07-23
/ PRIOR APPLICATION NUMBER: JP 2000-504165
/ PRIOR FILING DATE: 2000-01-24
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 47
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (1)..(9)
US-10-623-176-47
```

```
Query Match      76.3%; Score 29; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 DDLEA 9
        | | | | |
Db      2 DDLEA 7
```

```
RESULT 12
US-10-623-176-48
/ Sequence 48, Application US/10623176
/ Publication No. US20040092446A1
/ GENERAL INFORMATION:
/ APPLICANT: Goulmy, Els A.J.M.
/ APPLICANT: Hunt, Donald F.
/ APPLICANT: Engelhard, Victor H.
/ TITLE OF INVENTION: HA-1 epitopes and uses thereof
/ FILE REFERENCE: 2183-6047US
/ CURRENT APPLICATION NUMBER: US/10/623,176
/ CURRENT FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/489,760
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: EP 97202303.0
/ PRIOR FILING DATE: 1997-07-23
/ PRIOR APPLICATION NUMBER: PCT/NL98/00424
/ PRIOR FILING DATE: 1998-07-23
/ PRIOR APPLICATION NUMBER: JP 2000-504165
/ PRIOR FILING DATE: 2000-01-24
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 48
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
```

```
Query Match      76.3%; Score 29; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-48

Query Match 76.3%; Score 29; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLLEA 9
|||||
Db 2 DDLLEA 7

RESULT 13
US-10-623-176-23
Sequence 23, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Els A.J.M.
APPLICANT: Hunt, Donald F.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-23

Query Match 71.1%; Score 27; DB 15; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDL 7
|||||
Db 3 VLXDDL 9

RESULT 14
US-10-623-176-40
Sequence 40, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Els A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424

PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 40
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-40

Query Match 71.1%; Score 27; DB 15; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDL 7
|||||
Db 3 VLXDDL 9

RESULT 15
US-10-623-176-15
Sequence 15, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Els A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(8)
US-10-623-176-15

Query Match 60.5%; Score 23; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLLEA 9
|||||
Db 4 DLLEA 8

Search completed: December 29, 2004, 23:45:47
Job time : 162 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 23:22:17 ; Search time 38 Seconds
(without alignments)
22.788 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 38
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	42.1	7	2	S68004
2	16	42.1	8	2	PC4131
3	14	36.8	7	2	S20446
4	14	36.8	7	2	A59489
5	13	34.2	8	2	A61328
6	13	34.2	9	2	PH0942
7	13	34.2	9	2	A60427
8	12	31.6	4	2	I40697
9	12	31.6	5	2	PT0679
10	12	31.6	5	2	PT0601
11	12	31.6	6	2	B35640
12	12	31.6	6	2	PT0533
13	12	31.6	7	2	A34026
14	12	31.6	7	2	B39040
15	12	31.6	7	2	PT0628
16	12	31.6	7	2	PT0722
17	12	31.6	7	2	PT0576
18	12	31.6	8	2	PT0557
19	12	31.6	9	2	PH0108
20	12	31.6	9	2	PT0562
21	12	31.6	9	2	B30572
22	12	31.6	9	2	PS0253
23	11	28.9	6	2	T11779
24	11	28.9	7	2	S25266
25	11	28.9	8	2	S23428
26	11	28.9	8	2	B33099
27	11	28.9	8	2	S63165
28	11	28.9	8	2	PM0002
29	11	28.9	9	2	S66419

30	11	28.9	9	2	A12872	transaldolase (EC
31	11	28.9	9	2	A61386	macrophage inhibit
32	10	26.3	4	2	A48360	gamma subunit of p
33	10	26.3	4	2	A26209	protein-glutamine
34	10	26.3	6	2	H48394	glycoprotein compo
35	10	26.3	6	2	I48126	alpha-tubulin - Ch
36	10	26.3	7	2	S78024	ribosomal protein
37	10	26.3	7	2	A12016	formylglycinamide
38	10	26.3	7	2	C56793	platelet glycoprot
39	10	26.3	7	2	S29735	polyphosphate-gluc
40	10	26.3	7	2	PC2370	probable H+-transp
41	10	26.3	7	2	T09512	NADH2 dehydrogena
42	10	26.3	8	2	A32523	peptidyl-dipectida
43	10	26.3	8	2	T10077	hypothetical prote
44	10	26.3	8	2	PT0298	Ig heavy chain CRD
45	10	26.3	8	2	A42057	fibroblast growth

ALIGNMENTS

RESULT 1
S68004
hucolin, 75K chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S68004
R:Edgar, P.F.
PDBS Letc. 375, 159-161, 1995
A>Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
A:Reference number: S68004; MUID:96087107; PMID:7498469
A:Accession: S68004
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <EDG>

Query Match 42.1%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
DB 4 DDL 6

RESULT 2
PC4131
hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: PC4131
R:Kawasaki, S.; Arai, H.; Igatahi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A>Title: Sequencing and characterization of the downstream region of the genes encoding
Y for biosynthesis of heme dl.
A:Reference number: JC4552; MUID:96144254; PMID:8566817
A:Accession: PC4131
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <KAW>
A:Cross-references: UNIPROT:P5412; DDBJ:D50473; NID:g1217594
A>Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0

Query Match 42.1%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
DB 2 DDL 4

RESULT 3

S20446
elastase - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C:Accession: S20446
R:Kessler, B.; Saffin, M.; Peretz, M.; Burshtein, Y.
FBS Lett. 299, 291-293, 1992
A:Title: Identification of cleavage sites involved in proteolytic processing of Pseudom
A:Reference number: S20446; MUID:92183956; PMID:1544509
A:Accession: S20446
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <RES>

Query Match
Best Local Similarity 36.8%; Score 14; DB 2; Length 7;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLE 8
|||
Db 3 DLID 6

RESULT 4
A59489
protein kinase C inhibitor - rat (fragment)
C:Species: Rattus norvegicus
C:Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 25-Aug-2003
C:Accession: A59489
R:Negoro, M.
Submitted to the Protein Sequence Database, June 2003
A:Description: Purification of PKCI from rat liver.
A:Reference number: A59489
A:Accession: A59489
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <NEG>
A:Experimental source: strain Wistar, liver
A:Note: p-Hydroxyacetophenone-Sepharose binding protein

Query Match
Best Local Similarity 36.8%; Score 14; DB 2; Length 7;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLXD 5
|||
Db 2 IFEDD 6

RESULT 5
A61328
trypsin (EC 3.4.21.4) precursor - minke whale (fragment)
C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 03-Jul-2004
C:Accession: A61328
R:Brixteux-Gregoire, S.; Schyns, R.; Florkin, M.; Emmens, M.; Welling, G.W.; Beintema, J
Biochim. Biophys. Acta 386, 244-255, 1975
A:Title: N-terminal amino acid sequence of trypsinogen from the lesser rorqual, Balaenop
creas.
A:Reference number: A61328; MUID:75146765; PMID:1125273
A:Accession: A61328
A:Molecule type: protein
A:Residues: 1-8 <BRI>
A:Cross-references: UNIPROT:O7M390
C:Keywords: hydrolase; protein digestion; serine protease; zymogen
F:1-8/Domain: activation peptide #status experimental <RPT>

Query Match
Best Local Similarity 34.2%; Score 13; DB 2; Length 8;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXKD 5
|||

Db 3 IDDD 6

RESULT 6
PH0942
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0942
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0942
A:Molecule type: mRNA
A:Residues: 1-9 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A:Note: the authors translated the codon TGC for residue 2 as Ala
C:Keywords: T-cell receptor

Query Match
Best Local Similarity 34.2%; Score 13; DB 2; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LLE 8
|||
Db 5 LLE 7

RESULT 7
A60427
macrophage cytotoxicity-inducing factor, 29K - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: A60427
R:Jones, C.W.; Prince, C.A.; Williams, J.S.
Exp. Hematol. 19, 704-709, 1991
A:Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducin
A:Reference number: A60427; MUID:91372335; PMID:1909970
A:Accession: A60427
A:Molecule type: protein
A:Residues: 1-9 <JON>
A:Cross-references: UNIPROT:O7MAR5
A:Note: the sequence from the text on page 706 is inconsistent with that from page 708 i
C:Keywords: cytokine

Query Match
Best Local Similarity 34.2%; Score 13; DB 2; Length 9;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXD 4
|||
Db 4 VLKD 7

RESULT 8
I10697
biotin A - Citrobacter freundii (fragment)
C:Species: Citrobacter freundii
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I10697
R:Shuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A:Title: Transcriptional regulation and gene arrangement of Baccherichia coli, Citrobacte
A:Reference number: I10697; MUID:89006280; PMID:2971595
A:Accession: I10697
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: UNIPROT:P13071; GB:M21922; NID:G144434

Query Match
Best Local Similarity 31.6%; Score 12; DB 2; Length 4;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
Db 3 DD 4

RESULT 9

T-cell receptor beta chain V-D-J region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0679; PT0708

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; PMID:91277601; PMID:1711558

A:Accession: PT0679

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-5 <FE2>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-2J

A:Accession: PT0708

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-5 <FE2>

A:Experimental source: newborn thymus, strain BALB/c, 161-2B

C:Keywords: T-cell receptor

Query Match 31.6%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
Db 4 DD 5

RESULT 10

T-cell receptor beta chain V-D-J region (120-2K) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004

C:Accession: PT0601; PT0617; PT0694

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; PMID:91277601; PMID:1711558

A:Accession: PT0601

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FE2>

A:Cross-references: UNIPROT:Q64512

A:Experimental source: newborn thymus, strain BALB/c, clone 120-2K

A:Accession: PT0617

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FE3>

A:Experimental source: newborn thymus, strain BALB/c, 120-2CA

A:Accession: PT0694

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-5 <FE2>

A:Experimental source: day 18 fetal thymus, strain BALB/c, 154-1H

C:Keywords: T-cell receptor

Query Match 31.6%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
Db 4 DD 5

RESULT 11

cerebellar degeneration-related protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993

C:Accession: B35640

R:Chen, Y.T.; Retig, W.U.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.B.

Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990

A:Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal mar

A:Reference number: A35640; PMID:90222173; PMID:2326268

A:Accession: B35640

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-6 <CHE>

Query Match 31.6%; Score 12; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
Db 3 EDL 5

RESULT 12

T-cell receptor beta chain V-D-J region (126-1A) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0533

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; PMID:91277601; PMID:1711558

A:Accession: PT0533

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-6 <FE2>

A:Experimental source: adult thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 31.6%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
Db 4 DD 5

RESULT 13

acetylcholinesterase (EC 3.1.1.7) 5.6S form - Pacific electric ray (fragment)

C:Species: Torpedo californica (Pacific electric ray)

C:Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996

C:Accession: A34026

R:Gidney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedrick, T.; Low, M.G.; Taylor, S.S.; 1

J. Biol. Chem. 263, 1140-1145, 1988

A:Title: Divergence in primary structure between the molecular forms of acetylcholineste

A:Reference number: A34026; PMID:88087239; PMID:3335534

A:Accession: A34026

A:Molecule type: protein

A:Residues: 1-7 <GIB>

A:Keywords: alternative splicing; carboxylic ester hydrolase

Query Match 31.6%; Score 12; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LEEA 9
Db 6 LEEA 9

Db 1 LIMA 4

RESULT 14

B39040
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C:Accession: B39040
R:Caia, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A:Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein
A:Reference number: A39040; MUID:91093153; PMID:1985907
A:Accession: B39040
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-7 <CAL>
C:Keywords: phosphoprotein; skeletal muscle

Query Match 31.6%; Score 12; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5

Db 1 DD 2

RESULT 15

PT0628
T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0628
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0628
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-7 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 31.6%; Score 12; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5

Db 4 DD 5

Search completed: December 29, 2004, 23:33:55
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 23:14:21 ; Search time 186 Seconds
(without alignments)
27.841 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 38
Sequence: 1 VLXDDLRA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1598

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	42.1	9	2 Q70SM2	Q70SM2 homo sapien
2	16	42.1	9	2 Q8LPT5	Q8LPT5 zea mays (m
3	16	42.1	9	2 P82568	P82568 streptococc
4	16	42.1	9	2 CAD79467	CAD79467 homo sapi
5	15	39.5	9	2 Q9XJN0	Q9XJN0 bacterioph
6	14	36.8	9	2 Q9FSZ2	Q9FSZ2 cicier arlet
7	14	36.8	9	2 Q9QZAB	Q9QZAB mus musculu
8	14	36.8	9	2 Q85710	Q85710 rous sarcom
9	14	36.8	9	2 Q8UTD7	Q8UTD7 human immun
10	13	34.2	7	2 Q99182	Q99182 gnatholebia
11	13	34.2	8	2 Q6U7R2	Q6U7R2 cryptococcu
12	13	34.2	8	2 Q9HDS4	Q9HDS4 aspergillus
13	13	34.2	8	2 Q7M390	Q7M390 balaenopter
14	13	34.2	8	2 Q8H9X1	Q8H9X1 bacterioph
15	13	34.2	8	2 Q8SBJ0	Q8SBJ0 bacterioph
16	13	34.2	8	2 Q63C68	Q63C68 glycine max
17	13	34.2	8	2 P72279	P72279 rhodococcus
18	13	34.2	8	2 Q51594	Q51594 plasmid col
19	13	34.2	8	2 AAQ88127	AAQ88127 cryptococ
20	13	34.2	8	2 AAT01227	AAT01227 glycine m
21	13	34.2	9	2 Q7M4R5	Q7M4R5 homo sapien
22	13	34.2	9	2 Q9B0T4	Q9B0T4 homo sapien
23	13	34.2	9	2 Q6Q7G0	Q6Q7G0 rana ridib
24	13	34.2	9	2 Q6UVK2	Q6UVK2 malus domes
25	13	34.2	9	2 Q91IX6	Q91IX6 macaca neme
26	13	34.2	9	2 Q8AUM7	Q8AUM7 carassius a
27	13	34.2	9	2 AAQ57275	AAQ57275 malus dom
28	13	34.2	9	2 AAT01544	AAT01544 rana ridi
29	13	34.2	9	2 AAT01545	AAT01545 rana ridi
30	13	34.2	9	2 AAT01546	AAT01546 rana ridi
31	13	34.2	9	2 AAT01547	AAT01547 rana ridi

32	13	34.2	9	2 AAT01548	AAT01548 rana ridi
33	13	34.2	9	2 AAT01549	AAT01549 rana ridi
34	13	34.2	9	2 AAT01550	AAT01550 rana ridi
35	13	34.2	9	2 AAT01551	AAT01551 rana ridi
36	13	34.2	9	2 AAT01552	AAT01552 rana ridi
37	13	34.2	9	2 AAT01553	AAT01553 rana ridi
38	13	34.2	9	2 AAT01554	AAT01554 rana ridi
39	13	34.2	9	2 AAT01555	AAT01555 rana ridi
40	13	34.2	9	2 AAT01556	AAT01556 rana ridi
41	13	34.2	9	2 AAT01557	AAT01557 rana ridi
42	13	34.2	9	2 AAT01558	AAT01558 rana ridi
43	13	34.2	9	2 AAT01559	AAT01559 rana ridi
44	13	34.2	9	2 AAT01560	AAT01560 rana ridi
45	12	31.6	5	1 B10A_CITFR	P13071 Citrobacter

ALIGNMENTS

RESULT 1					
Q70SM2	PRELIMINARY;	PRT;	9 AA.		
AC Q70SM2;					
DT 05-JUL-2004 (TrEMBLrel. 27, Created)					
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)					
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)					
DE Hypermethylation in cancer 1 (Fragment).					
GN Name=H1C1;					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX NCBI_Taxid=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Mammary gland;					
RA Pine S., Guerardel C., Deltour S., Godwin A.K., Leprieux D.;					
RT "Identification of a second G-C-rich promoter conserved in the human,					
RT murine and rat tumor suppressor genes H1C1.";					
RT Oncogene 23:4023-4031 (2004).					
DR EMBL: AJ550615; CAD79467.1; --					
FT NON_TER					
SQ SEQUENCE 9 AA; 964 MW; 5B5E6DB1681AA7 CRC64;					
Query Match	42.1%;	Score 16;	DB 2;	Length 9;	
Best Local Similarity	60.0%;	Pred. No. 1.8e+06;			
Matches 3;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;	
Qy 5 DLEA 9					
Db 3 DTMEA 7					
RESULT 2					
Q8LPT5	PRELIMINARY;	PRT;	9 AA.		
AC Q8LPT5;					
DT 01-OCT-2002 (TrEMBLrel. 22, Created)					
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)					
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)					
DE Beta-expansin-like protein (Fragment).					
OS Zea mays (Maize).					
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;					
OC PACAD clade: Panicoideae; Andropogoneae; Zea.					
OX NCBI_Taxid=4577;					
RN [1]					
RP SEQUENCE FROM N.A.					
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,					
RA Morgante M., Rafalski J.A.;					
RT Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.					
DR EMBL: AY094310; AAM21836.1; --					
FT NON_TER					
SQ SEQUENCE 9 AA; 977 MW; 5C05B2D2CB1AAA3 CRC64;					

Query Match 42.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 1.8e+06;
 Matches 2; Conservative 4; Mismatches 0; Indels 0;

QY 4 DDLEA 9
 ||::||
 DB 4 DEVDA 9

RESULT 3

P82568 PRELIMINARY; PRT; 9 AA.
 AC P82568;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxId=1314;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC STRAIN=CRS4;
 RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
 RA Vanbogaellen R.A.;
 RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
 proteins";
 RL Submitted (MAY-2000) to Swiss-Prot.
 CC -1- MASS SPECTROMETRY; MW=22592.04; METHOD=Electrospray.
 FT NON TER 1
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match 42.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 3; Mismatches 0; Indels 0;

QY 4 DDLE 8
 ||::||
 DB 4 DEVIE 8

RESULT 4

CAD79467 PRELIMINARY; PRT; 9 AA.
 AC CAD79467;
 DT 01-JUN-2004 (TREMBLrel. 27, Created)
 DT 01-JUN-2004 (TREMBLrel. 27, Last sequence update)
 DT 01-JUN-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypermethylated in cancer 1 (Fragment).
 GN HIC1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX PubMed=15007385;
 RA Pinte S., Guevarrel C., Delbour S., Godwin A.K., Leprience D.,
 RT "Identification of a second G-C-rich promoter conserved in the human,
 RL murine and rat tumor suppressor genes HIC1.";
 DR EMBL; AJ550616; CAD79467.1; -.
 FT NON TER 9
 FT NON TER 9
 SQ SEQUENCE 9 AA; 964 MW; 5B5E6DB1681AA7 CRC64;

Query Match 42.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DLEA 9
 ||::||
 DB 3 DTMEA 7

RESULT 5

O9XJNO PRELIMINARY; PRT; 9 AA.
 AC O9XJNO;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE P10 (Fragment).
 OS Bacteriophage phi-10.
 OC Viruses; dsRNA viruses; Cystoviridae; Cystovirus.
 OX NCBI_TaxId=90889;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99350412; PubMed=10419946;
 RA Mindich L., Qiao X., Qiao J., Onodera S., Romantschuk M.,
 RA Hoogstraaten D.;
 RT "Isolation of additional bacteriophages with genomes of segmented
 RL double-stranded RNA.";
 DR EMBL; AF125675; AAD2255.1; -.
 FT NON TER 9
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1058 MW; 880E376AA720544A CRC64;

Query Match 39.5%; Score 15; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 3; Mismatches 0; Indels 0;

QY 4 DDLE 8
 ||::||
 DB 2 DNILD 6

RESULT 6

O9FSZ2 PRELIMINARY; PRT; 9 AA.
 AC O9FSZ2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Cicer arvense (Chickpea) (Garbanzo).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
 OX NCBI_TaxId=3827;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Etolated epicotyls;
 RA Dopico B., Jimenez T., Labrador E.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ299069; CAC10216.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 9 AA; 990 MW; 9441BDDA7272B8E CRC64;

Query Match 36.8%; Score 14; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LLEA 9
 ||::||
 DB 4 LLDA 7

RESULT 7

O9QZAB PRELIMINARY; PRT; 9 AA.
 AC O9QZAB;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE P10 (Fragment).
 OS Bacteriophage phi-10.
 OC Viruses; dsRNA viruses; Cystoviridae; Cystovirus.
 OX NCBI_TaxId=90889;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99350412; PubMed=10419946;
 RA Mindich L., Qiao X., Qiao J., Onodera S., Romantschuk M.,
 RA Hoogstraaten D.;
 RT "Isolation of additional bacteriophages with genomes of segmented
 RL double-stranded RNA.";
 DR EMBL; AF125675; AAD2255.1; -.
 FT NON TER 9
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1058 MW; 880E376AA720544A CRC64;

```

DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE C-type lectin DC11 (Fragment).
GN Name=DC11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA Gorzki K., Huang X., Tseng S.-Y., Rattis F., Pardoll D., Tsuchiya H.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF192526; AAF04843.1; -.
DR MGD; MGI:2136650; Dc11.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0046703; F:natural killer cell lectin-like receptor bi. .; IDA.
DR GO; GO:0005515; F:protein binding; IPT.
KM Lectin.
FT NON TER
SQ SEQUENCE 9 AA; 994 MW; 342161AB172EBAB7 CRC64;

Query Match
Best Local Similarity 36.8%; Score 14; DB 2; Length 9;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DLE 8
| | |
| | |
DB 3 DCLE 6

RESULT 8
ID 085710 PRELIMINARY; PRT; 9 AA.
AC Q85710;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Pol protein (Fragment).
OS Rous sarcoma virus.
OC Viruses; Retrovirdae; Retroviridae; Alpharetrovirus.
OC NCBI_TaxID=11886;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=84115080; PubMed=6319754;
RA Lerner T.L., Hanafusa H.;
RT "DNA sequence of the Bryan high-titer strain of Rous sarcoma virus:
RT extent of env deletion and possible genealogical relationship with
RT other viral strains.";
RL J. Virol. 49:549-556(1984).
DR EMBL; K03365; AAA42557.1; -.
FT NON TER
SQ SEQUENCE 9 AA; 949 MW; 94AA144DDDD731AA CRC64;

Query Match
Best Local Similarity 36.8%; Score 14; DB 2; Length 9;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 DDL 9
| | |
| | |
DB 1 EDT1AA 6

RESULT 9
ID 08UTD7 PRELIMINARY; PRT; 9 AA.
AC Q8UTD7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Vpu protein.
GN Name=vpu;
OS Human immunodeficiency virus 1.

```

```

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21988475; PubMed=11991972;
RA Novitsky V., Smith U.R., Gilbert P., McLane M.F., Chigwedere P.,
RA Williamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T., Thior I.,
RA Foley B.T., Gaoletwe S., Rybak N., Gaselstwe S., Vanberg F.,
RA Marink R., Lee T.-H., Essex M.;
RT "Human immunodeficiency virus type 1 subtype C molecular phylogeny:
RT consensus sequence for an AIDS vaccine design?";
RL J. Virol. 76:5435-5451(2002).
[2]
RP SEQUENCE FROM N.A.
RA Novitsky V.A., McLane M.F., Chigwedere P., Ndung'u T., Klein I.,
RA Chang S.-Y., Peter T., Thior I., Rybak N., Gaselstwe S., Vanberg F.,
RA Marink R., Lee T.-H., Essex M.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF443091; AAL34712.1; -.
SQ SEQUENCE 9 AA; 1102 MW; 188BD40B17272440 CRC64;

Query Match
Best Local Similarity 36.8%; Score 14; DB 2; Length 9;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLE 8
| | |
| | |
DB 3 NLE 6

RESULT 10
ID 099182 PRELIMINARY; PRT; 7 AA.
AC 099182;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN Name=COI;
OS Gnatholebias zonatus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnathobias.
RN NCBI_TaxID=135316;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20072928; PubMed=10603257;
RA Murphy W.J., Thomsen J.E., Collier G.E.;
RT "Phylogeny of the Neotropical Killifish family Rivulidae
RT (Cyprinodontiformes, Aplocheilidae) inferred from mitochondrial DNA
RT sequences.";
RL Mol. Phylogenet. Evol. 13:289-301(1999).
DR EMBL; AF002591; AAD01074.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON TER
SQ SEQUENCE 7 AA; 899 MW; 672721F6C8572030 CRC64;

Query Match
Best Local Similarity 34.2%; Score 13; DB 2; Length 7;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VLXDDL 7
| | |
| | |
DB 1 ILYQHL 7

RESULT 11
ID 06UTR2 PRELIMINARY; PRT; 8 AA.
AC 06UTR2;

```

DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Squalene monooxygenase (EC 1.14.99.7) (Fragment).
 GN Name=ERG1.
 OS Cryptococcus neoformans var. grubii H99.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremelliomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=235443;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H99;
 RA Stuart L.T., Allen A., Dietrich F.S.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY376718; AAQ88127.1; -.
 DR GO; GO:0004506; F:squalene monooxygenase activity; IEA.
 KW Monooxygenase; Oxidoreductase.
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 811 MW; 0467776AAB1D727 CRC64;

Query Match 34.2%; Score 13; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDD 5
 :|:
 Db 1 LLAED 5

RESULT 12

ID Q9HDS4 PRELIMINARY; PRT; 8 AA.
 AC Q9HDS4;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE TrpC polypeptide (Fragment).
 GN Name=trpC;
 OS Aspergillus flavus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5059;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A55;
 RC MEDLINE=21173963; PubMed=11273679;
 RA Geisler D.M., Dörner J.W., Horn B.W., Taylor J.W.;
 RT "The phylogenetics of mycotoxin and sclerotium production in
 RT Aspergillus flavus and Aspergillus oryzae.";
 RL Fungal Genet. Biol. 31:169-179(2000).
 DR EMBL; AF261861; AAG16135.1; -.
 KW Polypeptide.
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 807 MW; F3B2C72AB5B87DD6 CRC64;

Query Match 34.2%; Score 13; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLLE 8
 :|:
 Db 5 DLVD 8

RESULT 13

ID Q7M390 PRELIMINARY; PRT; 8 AA.
 AC Q7M390;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Trypsin (EC 3.4.21.4) precursor (Fragment). (Lesser rorqual).
 OS Balaenoptera acutorostrata (Minke whale).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaenopteridae; Balaenoptera.
 OX NCBI_TaxID=9767;
 RN [1]
 RP SEQUENCE.
 RA Briteux-Gregoire S., Schyns R., Florquin M., Emmens M., Welling G.W.,
 RA Belintema J.J.;
 RT "N-terminal amino acid sequence of trypsinogen from the lesser
 RT rorqual, Balaenoptera acutorostrata (Cetacea). Simultaneous isolation
 RT of trypsinogen, chymotrypsinogen and ribonuclease from pancreas.";
 RL Biochim. Biophys. Acta 386:244-255(1975).
 DR PIR; A61328; A61328.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 964 MW; 8D3A8AAAAA04769 CRC64;

Query Match 34.2%; Score 13; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXDD 5
 :|:
 Db 3 IDDD 6

RESULT 14

ID Q8H9X1 PRELIMINARY; PRT; 8 AA.
 AC Q8H9X1;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Gp30.2 protein (Fragment).
 GN Name=30.2;
 OS Bacteriophage L210.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC T4-like viruses.
 OX NCBI_TaxID=192973;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kolesinskiene G., Nivinskas R.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ458400; CAD30256.1; -.
 FT NON TER 8 8
 SQ SEQUENCE 8 AA; 918 MW; F3B1A72041B76336 CRC64;

Query Match 34.2%; Score 13; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXD 4
 :|:
 Db 5 ILTD 8

RESULT 15

ID Q8SB0 PRELIMINARY; PRT; 8 AA.
 AC Q8SB0;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Gp30.2 (Fragment).
 GN Name=30.2;
 OS Bacteriophage RB69.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC T4-like viruses.
 OX NCBI_TaxID=12353;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Plesniene L., Kolesinskiene G., Truncatė L., Zajackauskaitė A.,

RA Nivinskas R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ439452; CAD28423.1; -
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 918 MW; F3B1A72041B76336 CRC64;

Query Match 34.2%; Score 13; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLXD 4
 : | |
 Db 5 ILTD 8

Search completed: December 29, 2004, 23:33:08
 Job time : 191 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 22:57:00 ; Search time 151 Seconds
(without alignment) 21.381 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 38
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	94.7	9	2 AAW99195	AAW99195 Minor his
2	36	94.7	9	2 AAW99196	AAW99196 Minor his
3	36	94.7	9	2 AAW99197	AAW99197 Minor his
4	36	94.7	9	2 AAW97572	AAW97572 T-cell ep
5	36	94.7	9	2 AAW97375	AAW97375 HA-1 H-a1
6	36	94.7	9	2 AAW97374	AAW97374 HA-1 R-a1
7	36	94.7	9	8 ADH40333	ADH40333 Human min
8	36	94.7	9	8 ADH40334	ADH40334 Human min
9	36	94.7	13	2 AAW99199	AAW99199 VR cell K
10	36	94.7	13	2 AAW99198	AAW99198 DH cell K
11	36	94.7	13	2 AAW97415	AAW97415 KIAA0223
12	36	94.7	13	2 AAW97414	AAW97414 KIAA0223
13	36	94.7	1136	5 ADI17193	ADI17193 Human NOV
14	36	94.7	1136	5 ADI16744	ADI16744 Human NOV
15	36	94.7	1136	8 ADH61299	ADH61299 INTSG PR
16	36	94.7	1136	8 ADH42358	ADH42358 Human nov
17	36	94.7	1165	5 ADI17194	ADI17194 Human NOV
18	36	94.7	192	2 AAW34986	AAW34986 Chlamydia
19	36	94.7	226	4 AAW53226	AAW53226 Propionib
20	36	94.7	226	6 ABM49745	ABM49745 Propionib
21	36	94.7	499	5 ABB90575	ABB90575 Chlamydia
22	36	94.7	499	6 ABB26874	ABB26874 Protein e
23	36	94.7	635	7 ABO82267	ABO82267 Pseudomon
24	36	94.7	4150	3 AAY92707	AAY92707 S. antiB1
25	36	94.7	149	3 AAB25210	AAB25210 Eucalyptu

26	31	81.6	276	5 ABB48245	ABB48245 Listeria
27	31	81.6	289	5 AAU72987	AAU72987 Neisseria
28	31	81.6	289	5 AAU73000	AAU73000 Neisseria
29	31	81.6	289	5 ABB91578	ABB91578 Purine/py
30	31	81.6	289	5 ABB91584	ABB91584 Purine/py
31	31	81.6	289	6 ABB77961	ABB77961 N. gonorr
32	31	81.6	289	6 ABB37265	ABB37265 Protein e
33	31	81.6	289	6 ABB37881	ABB37881 Protein e
34	31	81.6	665	6 ABB31214	ABB31214 Protein e
35	31	81.6	675	6 ABB28302	ABB28302 Protein e
36	31	81.6	1042	4 ABB59345	ABB59345 Drosophila
37	31	81.6	1177	6 ABB71254	ABB71254 Chimeric
38	31	81.6	1186	6 ABB71253	ABB71253 Zebrafish
39	30	78.9	94	4 AAU86478	AAU86478 Novel hum
40	30	78.9	94	7 ADB59812	ADB59812 Connectiv
41	30	78.9	117	8 ADI48890	ADI48890 OIL-asoc
42	30	78.9	162	8 ADI20159	ADI20159 Human PRO
43	30	78.9	328	4 AAG73861	AAG73861 Human COL
44	30	78.9	423	6 ABB21143	ABB21143 Protein e
45	30	78.9	454	7 ABO64879	ABO64879 Klebsiella

ALIGNMENTS

RESULT 1	AAW99195	standard; peptide; 9 AA.
ID	AAW99195	
AC	AAW99195;	
DT	20-MAY-1999	(first entry)
DE	Minor histocompatibility antigen HA-1 T-cell epitope #1.	
XX	Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;	
KW	graft versus host disease; bone marrow transplant; leukaemia; vaccine;	
KM	diagnosis; aplastic anaemia; immune deficiency disease.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
FH	Key	Location/Qualifiers
FT	Misc-difference 3	/label= His, Arg
FT		
XX	W09905174-A1.	
XX		
PD	04-FEB-1999.	
XX		
XX	23-JUL-1998;	98MO-NL000425.
PF		
XX	23-JUL-1997;	97BP-00202303.
PR		
XX	(UYLE-) RICKSUNITV LEIDEN.	
XX		
PI	Goulmy EAMV, Hunt DF, Engelhard VH;	
XX		
DR	WPI, 1999-15312/13.	
XX		
PT	A new minor histocompatibility antigen, HA-1 - useful to treat immune	
PT	diseases and prevent rejection and host versus graft disease in bone	
PT	marrow and organ transplantation.	
XX		
PS	Claim 1; Page 32; 47pp; English.	
XX		
CC	The present sequence represents a new peptide (P1) constituting a T-cell	
CC	epitope obtainable from the minor histocompatibility antigen HA-1. The	
CC	peptide is immunogenic and can be used as part of a vaccine. P1 is used	
CC	as a medicine, to induce tolerance for transplants, prevent rejection	
CC	and/or graft versus host disease, or to treat (auto) immune diseases. In	
CC	particular it can be used with bone marrow transplantation, in the	
CC	treatment of severe aplastic anaemia, leukaemia, and immune deficiency	

```

CC diseases
SQ Sequence 9 AA;

Query Match
Best Local Similarity 94.7%; Score 36; DB 2; Length 9;
Matches 9; Conservative 100.0%; Pred. No. 1.7e+06; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
   |||||
Db 1 VLHDDLLEA 9

RESULT 2
AAW99196
ID AAW99196 standard; peptide; 9 AA.
AC AAW99196;
XX
XX
XX 20-MAY-1999 (first entry)
DE Minor histocompatibility antigen HA-1 T-cell epitope #2.
XX
XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
XX graft versus host disease; bone marrow transplant; leukaemia; vaccine;
XX diagnosis; aplastic anaemia; immune deficiency disease.
XX
XX Homo sapiens.
XX
XX WO9905174-A1.
XX
XX 04-FEB-1999.
XX
XX 23-JUL-1998; 98WO-NL000425.
XX
XX 23-JUL-1997; 97EP-00202303.
XX
XX (UYLE-) RIKKSUNIV LEIDEN.
XX
XX PA
XX PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
XX WPI; 1999-153312/13.
XX
XX DR
XX
XX A new minor histocompatibility antigen, HA-1 - useful to treat immune
XX diseases and prevent rejection and host versus graft disease in bone
XX marrow and organ transplantation.
XX
XX Claim 3; Page 32; 47pp; English.
XX
XX PS
XX
XX The present sequence represents a new peptide (P1) constituting a T-cell
XX epitope obtainable from the minor histocompatibility antigen HA-1. The
XX peptide is immunogenic and can be used as part of a vaccine. P1 is used
XX as a medicine, to induce tolerance for transplants, prevent rejection
XX and/or graft versus host disease, or to treat (auto) immune diseases. In
XX particular it can be used with bone marrow transplantation, in the
XX treatment of severe aplastic anaemia, leukaemia, and immune deficiency
XX diseases
XX
XX CC
XX
XX SQ Sequence 9 AA;

Query Match
Best Local Similarity 94.7%; Score 36; DB 2; Length 9;
Matches 8; Conservative 88.9%; Pred. No. 1.7e+06; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
   |||||
Db 1 VLHDDLLEA 9

RESULT 3
AAW99197
ID AAW99197 standard; peptide; 9 AA.
XX

```

```

AC AAW99197;
XX
XX 20-MAY-1999 (first entry)
DE Minor histocompatibility antigen HA-1 T-cell epitope #3.
XX
XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
XX graft versus host disease; bone marrow transplant; leukaemia; vaccine;
XX diagnosis; aplastic anaemia; immune deficiency disease.
XX
XX Homo sapiens.
XX
XX WO9905174-A1.
XX
XX 04-FEB-1999.
XX
XX 23-JUL-1998; 98WO-NL000425.
XX
XX 23-JUL-1997; 97EP-00202303.
XX
XX (UYLE-) RIKKSUNIV LEIDEN.
XX
XX PA
XX PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
XX WPI; 1999-153312/13.
XX
XX DR
XX
XX A new minor histocompatibility antigen, HA-1 - useful to treat immune
XX diseases and prevent rejection and host versus graft disease in bone
XX marrow and organ transplantation.
XX
XX Disclosure; Page 15; 47pp; English.
XX
XX PS
XX
XX The present sequence represents a new peptide (P1) constituting a T-cell
XX epitope obtainable from the minor histocompatibility antigen HA-1. The
XX peptide is immunogenic and can be used as part of a vaccine. P1 is used
XX as a medicine, to induce tolerance for transplants, prevent rejection
XX and/or graft versus host disease, or to treat (auto) immune diseases. In
XX particular it can be used with bone marrow transplantation, in the
XX treatment of severe aplastic anaemia, leukaemia, and immune deficiency
XX diseases
XX
XX CC
XX
XX SQ Sequence 9 AA;

Query Match
Best Local Similarity 94.7%; Score 36; DB 2; Length 9;
Matches 8; Conservative 88.9%; Pred. No. 1.7e+06; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
   |||||
Db 1 VLHDDLLEA 9

RESULT 4
AAW97572
ID AAW97572 standard; peptide; 9 AA.
AC AAW97572;
XX
XX 20-MAY-1999 (first entry)
DE T-cell epitope from the minor histocompatibility antigen HA-1.
XX
XX T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
XX transplant rejection; Graft-versus-Host Disease; autoimmune disease;
XX neoplastic haematopoietic cell.
XX
XX KW
XX
XX OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FT Misc-difference 3 /note= "His or Arg"
XX
XX W09905173-A1.
XX
XX PN

```


XX 04-FEB-1999.
 PD 98WO-NL000424.
 XX 23-JUL-1998;
 XX 23-JUL-1997; 97EP-00202303.
 XX (UYLE-) RIJXSUNIV LEIDEN.
 XX
 XX Goulmy EAM, Hunt DF, Engelhard VH;
 XX WPI; 1999-142855/12.
 DR
 PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
 PT for inducing tolerance to transplants and prevent rejection or graft-
 PT versus-host disease.
 XX
 XX Claim 1; Page 39; 57pp; English.
 PS
 CC The present sequence represents an immunogenic peptide constituting a T-
 CC cell epitope, obtainable from the minor histocompatibility antigen HA-1.
 CC The peptide can be used in vaccines or pharmaceutical formulations as
 CC medicines to induce tolerance for transplants so as to prevent rejection
 CC and/or Graft-versus-Host Disease, or to treat autoimmune diseases.
 CC Neoplastic haematopoietic cells presenting the peptides, in an HLA class
 CC I context, can be eliminated after specific recognition of the peptides.
 CC The peptides can also be used to raise antibodies, T-cell receptor, B-
 CC and T-cells
 XX
 SQ Sequence 9 AA;

Query Match 94.7%; Score 36; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
 |||||
 Db 1 VLXDDLLEA 9

RESULT 5
 AAW97375
 ID AAW97375 standard; protein; 9 AA.
 XX
 XX AAW97375;
 AC
 XX 13-MAY-1999 (first entry)
 DT
 XX HA-1 H-allele sequence.
 DE
 XX Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KM R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KM severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO9905313-A2.
 PN
 XX 04-FEB-1999.
 PD
 XX 23-JUL-1998; 98WO-EP004928.
 PF
 XX 23-JUL-1997; 97EP-00202303.
 PR 02-JUN-1998; 98EP-00870125.
 XX
 XX (UYLE-) RIJXSUNIV LEIDEN.
 PA
 XX Goulmy E;
 PI
 XX WPI; 1999-142860/12.
 DR
 PT Typing minor histocompatibility antigen HA-1 - by amplifying and
 PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection

PT of genetic aberrances.
 XX
 XX Claim 18; Fig 5; 59pp; English.
 PS
 CC The present sequence represents part of the minor histocompatibility
 CC antigen HA-1 H-allele. The specification describes methods for typing
 CC alleles (preferably the H and R alleles) of the minor histocompatibility
 CC antigen HA-1 in a sample, which comprise detecting polymorphic
 CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
 CC methods can be used for HA-1 typing for bone marrow transplants, severe
 CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
 CC detection of genetic aberrances. The probes and primers of the invention
 CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
 CC anti-idiotypic B cells and/or T cells and antibodies
 XX
 SQ Sequence 9 AA;

Query Match 94.7%; Score 36; DB 2; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.7e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
 |||||
 Db 1 VLXDDLLEA 9

RESULT 6
 AAW97374
 ID AAW97374 standard; protein; 9 AA.
 XX
 XX AAW97374;
 AC
 XX 13-MAY-1999 (first entry)
 DT
 XX HA-1 R-allele sequence.
 DE
 XX Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
 KM R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
 KM severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO9905313-A2.
 PN
 XX 04-FEB-1999.
 PD
 XX 23-JUL-1998; 98WO-EP004928.
 PF
 XX 23-JUL-1997; 97EP-00202303.
 PR 02-JUN-1998; 98EP-00870125.
 XX
 XX (UYLE-) RIJXSUNIV LEIDEN.
 PA
 XX Goulmy E;
 PI
 XX WPI; 1999-142860/12.
 DR
 PT Typing minor histocompatibility antigen HA-1 - by amplifying and
 PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
 PT of genetic aberrances.
 XX
 XX Claim 13; Fig 5; 59pp; English.
 PS
 CC The present sequence represents part of the minor histocompatibility
 CC antigen HA-1 R-allele. The specification describes methods for typing
 CC alleles (preferably the H and R alleles) of the minor histocompatibility
 CC antigen HA-1 in a sample, which comprise detecting polymorphic
 CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
 CC methods can be used for HA-1 typing for bone marrow transplants, severe
 CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
 CC detection of genetic aberrances. The probes and primers of the invention
 CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
 CC anti-idiotypic B cells and/or T cells and antibodies

XX Sequence 9 AA;
SQ

Query Match	94.7%	Score 36	DB 2	Length 9
Best Local Similarity	88.9%	Pred. No. 1.7e+05		
Matches	8	Conservative	0	Mismatches 1
				Indels 0
				Gaps 0

QY	1	VLXDDLEA	9
Db	1	VLRDDLEA	9

```

RESULT 7
ADH40333
ID  ADH40333 standard; peptide; 9 AA.

```

AC ADH40333;

DT 11-MAR-2004 (first entry)

DE Human minor histocompatibility antigen HA-1 T cell epitope.

KM human, cytostatic; SNP profile; cancer; leukaemia
KM minor histocompatibility antigen; mHAg; T cell epitope.

OS Homo sapiens.

PN WO2003106692-A2.

PD 24-DEC-2003

PF 13-JUN-2003; 2003WO-EP006251.

PR 13-JUN-2002; 2002EP-00013423.

PA (MERE) MERCK PATENT GMBH.

PI Strittmatter W, Moll H;
.....

DR WPI; 2004-082200/08.

PT Providing allelic variant epitope of protein based on single nucleotide
PT polymorphism by defining target protein, screening database of protein,
PT identifying, selecting allelic variant protein, creating variant
PT epitopes.

PS Disclosure; Page 82; 119pp; English.

The invention relates to a novel method for providing epitopes of allelic variants of antigenic proteins from specific species based on single nucleotide polymorphism (SNP), by defining target protein/peptide or its subset, screening database of DNA encoding target protein, identifying, selecting allelic peptide/protein variants, expression product or its fragment encoded by DNA sequence having SNP, creating variant epitopes, selecting epitopes binding to MHC protein. A protein of the invention has cytostatic activity, and may have a use in a vaccine. The method is useful for generating a SNP profile of one or more individuals from a given species by applying the method for several protein from the individuals, where the SNP profile was related to disease, preferably cancer. This is useful for diagnosing a disease in an individual by generating the SNP-related polymorphic profile. A method of the invention is useful for transplanting haematopoietic stem cells from a donor to a recipient and treating cancer, preferably leukaemia, and for determining the progression, regression or onset of a treated disease. The present sequence is used in the exemplification of the invention.

SQ Sequence 9 AA;

Query Match	94.7%;	Score 36;	DB 8;	Length 9;
Best Local Similarity	88.9%;	Pred. No. 1.7e+06;		
Matches	8;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0

QY 1 VLXDDLLEA 9

Db 1 VLHDDLEEA 9

```

RESULT 8
ADH40334
ID    ADH40334 standard; peptide; 9 AA

```

AC ADH40334;

DT 11-MAR-2004 (first entry)

DE Human minor histocompatibility antigen HA-1 T cell epitope

KW human; cytostatic; vaccine; cancer; leukaemia;
KM minor histocompatibility antigen; mHAg; T cell epitope.

OS Homo sapiens.

PN WO2003106692-A2.

PD 24-DEC-2003.

PF 13-JUN-2003; 2003WO-EP006251.

PR 13-JUN-2002; 2002EP-00013423.

PA (MERE) MERCK PATENT GMBH.

PI Strittmatter W, Moll H;

DR WPI; 2004-082200/08.

PT providing allelic variant epitope of protein based on single nucleotide
PT polymorphism by defining target protein, screening database of protein,
PT identifying, selecting allelic variant protein, creating variant
PT epitopes.

PS Disclosure; Page 82; 119pp; English.

CC The invention relates to a novel method for providing epitopes of allelic
CC variants of antigenic proteins from specific target species based on single
CC nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC subset, screening database of DNA encoding target protein, identifying,
CC selecting allelic peptide/protein variants, expression product or its
CC fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC selecting epitopes binding to MHC protein. A product of the invention has
CC cytostatic activity, and may have a use in a vaccine. The method is
CC useful for generating a SNP profile of one or more individuals from a
CC given species by applying the method for several protein from the
CC individuals, where the SNP profile was related to disease, preferably
CC cancer. This is useful for diagnosing a disease in an individual by
CC generating the SNP-related polymorphic profile. A method of the invention
CC is useful for transplanting haematopoietic stem cells from a donor to a
CC recipient and treating cancer, preferably leukemia, and for determining
CC the progression, regression or onset of a treated disease. The present
CC sequence is used in the exemplification of the invention.

SQ Sequence 9 AA;

Query Match 94.7%; Score 36; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY      1 VLXDDLLEA $
         ||| |||||
Db      1 VLRDDLEEA $
```

RESULT 9	
AAW99199	
ID	AAW99199 standard; peptide; 13 AA

XX

AC AAW99199;
 XX 20-MAY-1999 (first entry)
 DT
 XX VR cell KIAA0223 protein sequence.
 DE
 XX Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
 KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
 KM diagnosis; aplastic anaemia; immune deficiency disease.
 XX
 OS Synthetic.
 XX
 PN WO9905174-A1.
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-NL000425.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 PI Goulmy EAJM, Hunt DF, Engelhard VH;
 XX
 DR WPI; 1999-153312/13.
 DR N-PSDB; AAX19409.
 XX
 PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
 PT diseases and prevent rejection and host versus graft disease in bone
 PT marrow and organ transplantation.
 PS
 XX Disclosure; Page 31; 47pp; English.
 CC
 CC The present invention describes a new peptide (P1) constituting a T-cell
 CC epitope obtainable from the minor histocompatibility antigen HA-1. The
 CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
 CC as a medicine, to induce tolerance for transplants, prevent rejection
 CC and/or graft versus host disease, or to treat (auto) immune diseases. In
 CC particular it can be used with bone marrow transplantation, in the
 CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
 CC diseases. The present sequence represents a KIAA0223 sequence given in
 CC the present invention
 CC
 XX
 SQ Sequence 13 AA;
 Query Match 94.7%; Score 36; DB 2; Length 13;
 Best Local Similarity 88.9%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 VLXDDLEA 9
 Db 3 VLHDDLEA 11
 RESULT 10
 AAW99198
 ID AAW99198 standard; peptide; 13 AA.
 XX
 AC AAW99198;
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE DH cell KIAA0223 protein sequence.
 XX
 KM Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
 KM graft versus host disease; bone marrow transplant; leukaemia; vaccine;
 KM diagnosis; aplastic anaemia; immune deficiency disease.
 XX
 OS Synthetic.
 XX
 PN WO9905174-A1.
 XX
 PD 04-FEB-1999.

XX 23-JUL-1998; 98WO-NL000425.
 PF
 XX 23-JUL-1997; 97EP-00202303.
 PR
 XX (UYLE-) RIJKSUNIV LEIDEN.
 PA
 XX Goulmy EAJM, Hunt DF, Engelhard VH;
 XX
 DR WPI; 1999-153312/13.
 DR N-PSDB; AAX19408.
 XX
 PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
 PT diseases and prevent rejection and host versus graft disease in bone
 PT marrow and organ transplantation.
 PS
 XX Disclosure; Page 31; 47pp; English.
 CC
 CC The present invention describes a new peptide (P1) constituting a T-cell
 CC epitope obtainable from the minor histocompatibility antigen HA-1. The
 CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
 CC as a medicine, to induce tolerance for transplants, prevent rejection
 CC and/or graft versus host disease, or to treat (auto) immune diseases. In
 CC particular it can be used with bone marrow transplantation, in the
 CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
 CC diseases. The present sequence represents a KIAA0223 sequence given in
 CC the present invention
 CC
 XX
 SQ Sequence 13 AA;
 Query Match 94.7%; Score 36; DB 2; Length 13;
 Best Local Similarity 88.9%; Pred. No. 1.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 VLXDDLEA 9
 Db 3 VLHDDLEA 11
 RESULT 11
 AAW97415
 ID AAW97415 standard; protein; 13 AA.
 XX
 AC AAW97415;
 XX
 DT 20-MAY-1999 (first entry)
 XX
 DE KIAA0223 polymorphism in HA-1 positive homozygous individuals.
 XX
 KM T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
 KM transplant rejection; Graft-versus-Host Disease; autoimmune disease;
 KM neoplastic haematopoietic cell; KIAA0223 polymorphism.
 XX
 OS Homo sapiens.
 XX
 PN WO9905173-A1.
 XX
 PD 04-FEB-1999.
 XX
 PF 23-JUL-1998; 98WO-NL000424.
 XX
 PR 23-JUL-1997; 97EP-00202303.
 XX
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 PI Goulmy EAJM, Hunt DF, Engelhard VH;
 XX
 DR WPI; 1999-142855/12.
 DR N-PSDB; AAX16081.
 XX
 PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
 PT for inducing tolerance to transplants and prevent rejection or graft-
 PT versus-host disease.

XX Disclosure; Page 38; 57pp; English.
XX
XX The present sequence represents the KIAA0223 polymorphism in HA-1
CC positive homozygous individuals. The specification describes an
CC immunogenic peptide constituting a T-cell epitope, obtainable from the
CC minor histocompatibility antigen HA-1. The peptide can be used in
CC vaccines or pharmaceutical formulations as medicines to induce tolerance
CC for transplants so as to prevent rejection and/or graft-versus-host
CC disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
CC presenting the peptides, in an HLA class I context, can be eliminated
CC after specific recognition of the peptides. The peptides can also be used
CC to raise antibodies, T-cell receptor, B- and T-cells
XX
SQ Sequence 13 AA;
Query Match 94.7%; Score 36; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VLXDDLLEA 9
Db 3 VLHDDLLEA 11
RESULT 12
AAW97414
ID AAW97414 standard; protein; 13 AA.
XX
XX AAW97414;
XX
XX 20-MAY-1999 (first entry)
XX
XX KIAA0223 polymorphism in HA-1 negative homozygous individuals.
DE T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
XX transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW neoplastic haematopoietic cell; KIAA0223 polymorphism.
XX
XX Homo sapiens.
OS W0905173-A1.
XX
XX 04-FEB-1999.
XX
XX 23-JUL-1998; 98WC-NL000424.
XX
XX 23-JUL-1997; 97EP-00202303.
XX
XX (UYLE-) RIKSUNIV LEIDEN.
XX
XX Goulmv EAJM, Hunt DF, Engelhard VH;
PI WPI, 1999-142855/12.
XX
XX N-PSDB; AAX16080.
XX
XX Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT for inducing tolerance to transplants and prevent rejection or graft-
XX versus-host disease.
XX
XX Disclosure; Page 38; 57pp; English.
XX
XX The present sequence represents the KIAA0223 polymorphism in HA-1
CC negative homozygous individuals. The specification describes an
CC immunogenic peptide constituting a T-cell epitope, obtainable from the
CC minor histocompatibility antigen HA-1. The peptide can be used in
CC vaccines or pharmaceutical formulations as medicines to induce tolerance
CC for transplants so as to prevent rejection and/or Graft-versus-Host
CC disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
CC presenting the peptides, in an HLA class I context, can be eliminated
CC after specific recognition of the peptides. The peptides can also be used
CC to raise antibodies, T-cell receptor, B- and T-cells
XX

SQ Sequence 13 AA;
Query Match 94.7%; Score 36; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VLXDDLLEA 9
Db 3 VLHDDLLEA 11
RESULT 13
AD117193
ID AD117193 standard; protein; 1136 AA.
XX
XX AD117193;
XX
XX 15-APR-2004 (first entry)
XX
XX Human NOVX protein homologue SegID 729.
DE human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; ascuma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; str.
XX
XX Homo sapiens.
OS W0200268649-A2.
XX
XX W0200268649-A2.
XX
XX 06-SEP-2002.
XX
XX 31-JAN-2002; 2002WC-US002785.
XX
XX 31-JAN-2001; 2001US-0265395P.
XX
XX 31-JAN-2001; 2001US-0265412P.
XX
XX 31-JAN-2001; 2001US-0265514P.
XX
XX 02-FEB-2001; 2001US-0266406P.
XX
XX 05-FEB-2001; 2001US-0266767P.
XX
XX 07-FEB-2001; 2001US-0266975P.
XX
XX 07-FEB-2001; 2001US-0267057P.
XX
XX 08-FEB-2001; 2001US-0267459P.
XX
XX 09-FEB-2001; 2001US-0267823P.
XX
XX 15-FEB-2001; 2001US-0271664P.
XX
XX 26-FEB-2001; 2001US-0271839P.
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XX 27-FEB-2001; 2001US-0271855P.
XX
XX 02-MAR-2001; 2001US-0272046P.
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XX 14-MAR-2001; 2001US-0275925P.
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XX 14-MAR-2001; 2001US-0275950P.
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XX 14-MAR-2001; 2001US-0275989P.
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XX 15-MAR-2001; 2001US-0276448P.
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XX 15-MAR-2001; 2001US-0276397P.
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XX 16-MAR-2001; 2001US-0276768P.
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XX 20-MAR-2001; 2001US-0278652P.
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XX 26-MAR-2001; 2001US-0278775P.
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XX 29-MAR-2001; 2001US-0279882P.
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XX 29-MAR-2001; 2001US-0280147P.
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XX 30-MAR-2001; 2001US-0282992P.
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XX 11-APR-2001; 2001US-02851083P.
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XX 20-APR-2001; 2001US-0285133P.
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XX 23-APR-2001; 2001US-0285749P.
XX
XX 03-MAY-2001; 2001US-0288327P.
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XX 03-MAY-2001; 2001US-0288504P.
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XX 29-MAY-2001; 2001US-0294047P.
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XX 30-MAY-2001; 2001US-0294473P.

PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.

(CURA-) CURAGEN CORP.
PI Tchernev VT, Spytek KA, Zerhusen BD, Patnirajan M, Shinkets RA;
PI Li L, Gangolli EA, Padigaru M, Anderson DM, Raetelli L, Miller CE;
PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
PI Furtak K, Grose WM, Albobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX WPI; 2002-706398/76.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Disclosure; SEQ ID NO 729; 1498bp; English.
XX
XX This invention relates to a novel nucleic acid, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC antiasthmatic, nephrotropic, antiarthritic, hepatotropic,
CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
CC of the invention.
XX
XX Sequence 1136 AA;
SQ

Query Match 94.7%; Score 36; DB 5; Length 1136;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
DB 137 VLRDDLEA 145

RESULT 14
AD116744

ID AD116744 standard; protein; 1136 AA.
XX
XX AC AD116744;
XX
XX DT 15-APR-2004 (first entry)
XX
XX DE Human NOVX protein to treat human pathological conditions SeqID280.
XX
XX KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KW inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
KW haemostatic; cardiant; antiinflammatory; immunosuppressive; antiallergic;
KW haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
KW antiasthmatic; nephrotropic; antiarthritic; hepatotropic;
KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
KW chromosome mapping; tissue typing; pharmacogenomic.
XX
XX OS Homo sapiens.
XX
XX PN WO200268649-A2.
XX
XX PD 06-SEP-2002.
XX
XX 31-JAN-2002; 2002WO-US002785.
XX
XX 31-JAN-2001; 2001US-0265395P.
XX 31-JAN-2001; 2001US-0265412P.
XX 31-JAN-2001; 2001US-0265514P.
XX 31-JAN-2001; 2001US-0265517P.
XX 02-FEB-2001; 2001US-0266406P.
XX 05-FEB-2001; 2001US-0266767P.
XX 07-FEB-2001; 2001US-0266975P.
XX 07-FEB-2001; 2001US-0267057P.
XX 08-FEB-2001; 2001US-0267459P.
XX 09-FEB-2001; 2001US-0267823P.
XX 15-FEB-2001; 2001US-0268974P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 27-FEB-2001; 2001US-0271855P.
XX 02-MAR-2001; 2001US-0272788P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275989P.
XX 15-MAR-2001; 2001US-0276448P.
XX 15-MAR-2001; 2001US-0276450P.
XX 16-MAR-2001; 2001US-0276397P.
XX 16-MAR-2001; 2001US-0276768P.
XX 20-MAR-2001; 2001US-0278652P.
XX 26-MAR-2001; 2001US-0278775P.
XX 26-MAR-2001; 2001US-0278782P.
XX 29-MAR-2001; 2001US-0279887P.
XX 29-MAR-2001; 2001US-0279884P.
XX 30-MAR-2001; 2001US-0280147P.
XX 11-APR-2001; 2001US-0282922P.
XX 11-APR-2001; 2001US-0283033P.
XX 20-APR-2001; 2001US-0285133P.
XX 23-APR-2001; 2001US-0285749P.
XX 03-MAY-2001; 2001US-0288327P.
XX 03-MAY-2001; 2001US-0288504P.
XX 29-MAY-2001; 2001US-0294047P.
XX 30-MAY-2001; 2001US-0294473P.
XX 08-JUN-2001; 2001US-0296959P.
XX 18-JUN-2001; 2001US-0296964P.
XX 19-JUN-2001; 2001US-0299324P.
XX 13-AUG-2001; 2001US-0312020P.
XX 16-AUG-2001; 2001US-0312889P.
XX 16-AUG-2001; 2001US-0312908P.
XX 21-AUG-2001; 2001US-0313390P.

PR 28-AUG-2001; 2001US-0315470P.
 PR 31-AUG-2001; 2001US-0316447P.
 PR 07-SEP-2001; 2001US-0318115P.
 PR 07-SEP-2001; 2001US-0318118P.
 PR 12-SEP-2001; 2001US-0318740P.
 PR 19-SEP-2001; 2001US-0323379P.
 PR 18-OCT-2001; 2001US-0330245P.
 PR 18-OCT-2001; 2001US-0330308P.
 PR 14-NOV-2001; 2001US-0332701P.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 PI Tchernev VT, Spytek KA, Zernhusen BD, Patumrajan M, Shinkets RA;
 PI Li L, Ganggoli EA, Padigaru M, Anderson DM, Rastelli L, Miller CE;
 PI Gerlach VT, Taupier RJ, Gusev VV, Colman SD, Wolenc AR, Pena CRA;
 PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
 XX
 DR MPI: 2002-706998/76.
 DR N-PSDB; ADI16743.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Claim 1; SEQ ID NO 280; 1499P; English.

CC This invention relates to a novel nucleic acid, and encoded polypeptides
 CC thereof, which have properties related to the stimulation of biochemical
 CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human and murine NOVX proteins, as well as methods to modulate their
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.
 CC The NOVX polypeptides, polynucleotides and antibodies are useful in
 CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
 CC treating or preventing diseases such as inflammation, autoimmune
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
 CC (AIDS), obesity, asthma, immunoglobulin (Ig) A nephropathy, cirrhosis,
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
 CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
 CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
 CC antiaesthetic, nephroprotective, antiarthritic, hepatocytotoxic, anorectic,
 CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a human NOVX protein of the
 CC invention.
 CC
 SQ Sequence 1136 AA;

Query Match 94.7%; Score 36; DB 5; Length 1136;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTXDDLEA 9
 DB 137 VLRDDLEA 145

RESULT 15

ID ADH61299 standard; protein; 1136 AA.

XX ADH61299;

XX 25-MAR-2004 (first entry)

DE INTSIG protein 7740249CD1, SEQ ID 16.

XX Cytostatic; anorectic; immunosuppressive; gene therapy;
 KW INTSIG-agonist; INTSIG-agonist; human;
 KW intracellular signaling molecule; INTSIG; autoimmune disorder; obesity;
 KW cancer.

OS Homo sapiens.

XX WO2004001005-A2.

XX 31-DEC-2003.

XX 18-JUN-2003; 2003WO-US019589.

XX 19-JUN-2002; 2002US-0390470P.

XX 16-AUG-2002; 2002US-0404235P.

XX 12-SEP-2002; 2002US-0410424P.

XX (INCY-) INCYTE CORP.

XX Li JX, Chawla NK, Gietzen KJ, Richardson TW, Kable AR;
 PI Ramkumar J, Elliott VS, Khare R, Ison CH, Bulloch SA, Yang J;
 PI Wilson AD, Griffin JA, Yang YG, Sprague WM, Tang YT;

XX MPI: 2004-082488/08.

XX N-PSDB; ADH61317.

PT New human intracellular signaling molecule (INTSIG) polypeptide, useful
 PT for preparing a composition for treating a disease associated with
 PT decreased expression or overexpression of functional INTSIG e.g., cancer.

XX Claim 1a; SEQ ID NO 16; 217P; English.

CC The invention relates to an isolated human intracellular signaling
 CC molecule (INTSIG) polypeptide. Also disclosed are the isolated
 CC polynucleotides encoding the polypeptides. The polypeptide is useful for
 CC preparing a composition for diagnosing or treating a disease or condition
 CC associated with decreased expression or overexpression of functional
 CC INTSIG e.g. autoimmune disorders, obesity or cancer. The current sequence
 CC represents an INTSIG polypeptide of the invention.
 CC
 SQ Sequence 1136 AA;

Query Match 94.7%; Score 36; DB 8; Length 1136;
 Best Local Similarity 88.9%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTXDDLEA 9
 DB 137 VLRDDLEA 145

Search completed: December 29, 2004, 23:09:37
 Job time : 155 secs

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OM protein - protein search, using sw model

Run on: December 29, 2004, 23:06:35 ; Search time 38 Seconds
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Title: US-10-791-217A-1
Perfect score: 38
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:
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6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	86.8	192	4	US-09-198-452A-404
2	32	84.2	635	4	US-09-252-991A-31013
3	32	84.2	4150	3	US-09-428-517-2
4	31	81.6	149	4	US-10-101-464A-529
5	30	78.9	454	4	US-09-489-039A-11396
6	30	78.9	776	4	US-09-252-991A-30380
7	30	78.9	822	4	US-09-886-319A-34
8	30	78.9	847	4	US-09-252-991A-29988
9	30	78.9	1410	3	US-09-335-409-3
10	30	78.9	1410	3	US-09-567-968-3
11	30	78.9	1410	3	US-09-567-968-3
12	30	78.9	1410	3	US-09-568-480-3
13	30	78.9	1410	3	US-09-568-486-3
14	30	78.9	1410	3	US-09-568-472-3
15	30	78.9	1410	3	US-09-567-899-3
16	29	76.3	142	4	US-09-248-796A-17805
17	29	76.3	199	4	US-09-543-681A-7115
18	29	76.3	259	4	US-09-252-991A-22086
19	29	76.3	263	4	US-09-252-991A-22624
20	29	76.3	410	4	US-09-489-039A-10283
21	29	76.3	413	4	US-09-489-039A-10299
22	29	76.3	415	4	US-09-583-110-4250
23	29	76.3	425	4	US-09-543-681A-7107
24	29	76.3	717	4	US-10-101-464A-810
25	29	76.3	1148	4	US-09-538-092-156
26	28	73.7	99	4	US-09-543-681A-8303
27	28	73.7	195	4	US-09-394-142B-16

28	28	73.7	251	5	PCT-US95-12357A-1	Sequence 1, Appli
29	28	73.7	252	4	US-09-506-286B-2	Sequence 2, Appli
30	28	73.7	252	4	US-09-506-286B-5	Sequence 5, Appli
31	28	73.7	252	4	US-09-762-861B-2	Sequence 2, Appli
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33	28	73.7	252	4	US-10-065-133A-2	Sequence 2, Appli
34	28	73.7	252	4	US-10-065-133A-5	Sequence 5, Appli
35	28	73.7	293	4	US-09-934-899-2	Sequence 2, Appli
36	28	73.7	293	4	US-09-934-899-2	Sequence 2, Appli
37	28	73.7	296	4	US-09-583-110-5143	Sequence 5143, Ap
38	28	73.7	334	4	US-09-489-039A-14107	Sequence 14107, A
39	28	73.7	550	1	US-08-674-168-29	Sequence 29, Appli
40	28	73.7	550	3	US-08-985-908-19	Sequence 19, Appli
41	28	73.7	550	3	US-08-852-730-4	Sequence 4, Appli
42	28	73.7	550	3	US-08-985-916-11	Sequence 11, Appli
43	28	73.7	605	4	US-09-270-767-46196	Sequence 46196, A
44	28	73.7	674	4	US-09-270-767-41618	Sequence 41618, A
45	28	73.7	679	4	US-09-270-767-44535	Sequence 44535, A

ALIGNMENTS

RESULT 1
US-09-198-452A-404
; Sequence 404, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 404
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-404

Query Match 86.8% ; Score 33; DB 4; Length 192;
Best Local Similarity 77.8% ; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 1 VLXDDLLEA 9
DB 88 VLXDDLLEA 96
RESULT 2
US-09-252-991A-31013
; Sequence 31013, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.116
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31013
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31013

Query Match 84.2%; Score 32; DB 4; Length 635;
Best Local Similarity 77.8%; Pred. No. 98;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
Db 119 VLADLLEA 127

RESULT 3

US-09-428-517-2
; Sequence 2, Application US/09428517
; Patent No. 6251636
; GENERAL INFORMATION:
; APPLICANT: Bectach, Mary C.
; APPLICANT: Shah, Sanjay Krishnakant
; APPLICANT: McDaniel, Robert
; APPLICANT: Tang, Li
; TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 30062-20029.00
; CURRENT APPLICATION NUMBER: US/09/428,517
; CURRENT FILING DATE: 1999-10-28
; EARLIER APPLICATION NUMBER: 60/120,254
; EARLIER FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/106,100
; EARLIER FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4150
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-2

Query Match 84.2%; Score 32; DB 3; Length 4150;
Best Local Similarity 87.5%; Pred. No. 8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXXDDLLEA 9
Db 1781 LRDDLLEA 1788

RESULT 4

US-10-101-464A-529
; Sequence 529, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 529
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Eucalyptus grandis

US-10-101-464A-529

Query Match 81.6%; Score 31; DB 4; Length 149;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
Db 73 ILDDLLEA 81

RESULT 5

US-09-489-039A-11396
; Sequence 11396, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11396
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11396

Query Match 78.9%; Score 30; DB 4; Length 454;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
Db 379 VLDDLLEA 387

RESULT 6

US-09-252-991A-30380
; Sequence 30380, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30380
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30380

Query Match 78.9%; Score 30; DB 4; Length 776;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXXDDLLEA 9
Db 618 LADLLEA 625

RESULT 7

US-09-886-319A-34

Sequence 34, Application US/09886319A
Patent No. 6586185
GENERAL INFORMATION:
APPLICANT: Wolf, Eckard
APPLICANT: Werner, Sabine
APPLICANT: Halle, Jörn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
FILE REFERENCE: 50125/014002
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 822
TYPE: PRT
ORGANISM: Homo sapiens
US-09-886-319A-34

Query Match 78.9%; Score 30; DB 4; Length 822;
Best Local Similarity 75.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLXDDLE 8
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Db 552 VLXDDLE 559

RESULT 8
US-09-252-991A-29988
Sequence 29988, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29988
LENGTH: 847
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29988

Query Match 78.9%; Score 30; DB 4; Length 847;
Best Local Similarity 75.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLXDDLE 8
|||:|
Db 189 VLXDDLE 196

RESULT 9
US-09-335-409-3
Sequence 3, Application US/09335409
Patent No. 6121029
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas

APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1410
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-335-409-3

Query Match 78.9%; Score 30; DB 3; Length 1410;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 LXXDDLEA 9
|||:|
Db 474 LXXDDLEA 481

RESULT 10
US-09-568-102-3
Sequence 3, Application US/09568102
Patent No. 6346404
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,102
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1410
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-568-102-3

Query Match 78.9%; Score 30; DB 3; Length 1410;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 LXXDDLEA 9
|||:|
Db 474 LXXDDLEA 481

RESULT 11
US-09-567-969-3
Sequence 3, Application US/09567969
Patent No. 6355457
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A

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; CURRENT APPLICATION NUMBER: US/09/567,969
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1410
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-567-969-3

Query Match          78.9%; Score 30; DB 3; Length 1410;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LKDDLLEA 9
DB      474 LKDDLLEA 481

RESULT 12
US-09-568-480-3
; Sequence 3, Application US/09568480
; Patent No. 6355458
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHLONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,480
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1410
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-480-3

Query Match          78.9%; Score 30; DB 3; Length 1410;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LKDDLLEA 9
DB      474 LKDDLLEA 481

RESULT 13
US-09-568-486-3
; Sequence 3, Application US/09568486
; Patent No. 6355459
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHLONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,486
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1410
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-486-3

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Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB      474 LKDDLLEA 481

RESULT 14
US-09-568-472-3
; Sequence 3, Application US/09568472
; Patent No. 6358719
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHLONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,472
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1410
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-472-3

Query Match          78.9%; Score 30; DB 3; Length 1410;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 LKDDLLEA 9
DB      474 LKDDLLEA 481

RESULT 15
US-09-567-899-3
; Sequence 3, Application US/09567899
; Patent No. 6383787
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHLONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/567,899
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1410
; TYPE: PRT
; ORGANISM: Sorangium cellulosum

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US-09-567-899-3

Query Match 78.9%; Score 30; DB 3; Length 1410;
 Best Local Similarity 75.0%; Pred. No. 6.3e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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 Db 474 LKDDMLBA 481

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OM protein - protein search, using sw model

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Title: US-10-791-217A-1
Perfect score: 38
Sequence: 1 VLXDDLLEA 9

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Gapop 10.0 , Gapext 0.5

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SUMMARIES

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2	36	94.7	9	US-10-623-176-2	Sequence 2, Appli
3	36	94.7	9	US-10-623-176-10	Sequence 10, Appli
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5	36	94.7	9	US-10-791-217-2	Sequence 2, Appli
6	36	94.7	9	US-10-791-217-5	Sequence 5, Appli
7	36	94.7	10	US-10-623-176-24	Sequence 24, Appli
8	36	94.7	10	US-10-623-176-43	Sequence 43, Appli
9	36	94.7	10	US-10-623-176-44	Sequence 44, Appli
10	36	94.7	12	US-10-623-176-65	Sequence 65, Appli
11	36	94.7	13	US-10-623-176-74	Sequence 74, Appli
12	36	94.7	13	US-10-623-176-76	Sequence 76, Appli
13	36	94.7	17	US-10-791-217-14	Sequence 14, Appli

14	36	94.7	13	17	US-10-791-217-16	Sequence 16, Appli
15	36	94.7	17	15	US-10-623-176-33	Sequence 33, Appli
16	36	94.7	17	15	US-10-623-176-57	Sequence 57, Appli
17	36	94.7	17	15	US-10-623-176-69	Sequence 69, Appli
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21	36	94.7	22	15	US-10-623-176-72	Sequence 72, Appli
22	36	94.7	23	15	US-10-623-176-72	Sequence 72, Appli
23	36	94.7	25	15	US-10-623-176-55	Sequence 55, Appli
24	36	94.7	25	15	US-10-623-176-67	Sequence 67, Appli
25	36	94.7	26	15	US-10-623-176-66	Sequence 66, Appli
26	36	94.7	27	15	US-10-623-176-51	Sequence 51, Appli
27	36	94.7	27	15	US-10-623-176-60	Sequence 60, Appli
28	36	94.7	28	15	US-10-623-176-61	Sequence 61, Appli
29	36	94.7	29	15	US-10-623-176-49	Sequence 49, Appli
30	36	94.7	29	15	US-10-623-176-59	Sequence 59, Appli
31	36	94.7	1136	15	US-10-072-012-280	Sequence 280, App
32	36	94.7	1136	15	US-10-072-012-729	Sequence 729, App
33	36	94.7	1165	15	US-10-072-012-730	Sequence 730, App
34	35	92.1	408	16	US-10-437-963-114620	Sequence 114620,
35	33	86.8	95	16	US-10-767-701-61761	Sequence 61761, A
36	33	86.8	185	14	US-10-156-761-8607	Sequence 8607, Ap
37	33	86.8	192	15	US-10-289-762-404	Sequence 404, App
38	33	86.8	218	17	US-10-425-115-225678	Sequence 225678,
39	33	86.8	297	15	US-10-425-114-73046	Sequence 73046, A
40	33	86.8	317	17	US-10-425-115-225676	Sequence 225676,
41	33	86.8	499	15	US-10-312-273-99	Sequence 99, Appli
42	33	86.8	499	15	US-10-282-122A-54798	Sequence 54798, A
43	32	84.2	9	15	US-10-623-176-41	Sequence 41, Appli
44	32	84.2	9	15	US-10-623-176-42	Sequence 42, Appli
45	32	84.2	9	15	US-10-623-176-45	Sequence 45, Appli

ALIGNMENTS

RESULT 1
US-10-623-176-1
Sequence 1, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Els A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT FILING DATE: US/10/623.176
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
NAME/KEY: SITE
LOCATION: (1)..(9)
US-10-623-176-1
Query Match 94.7%; Score 36; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|||||

Db 1 VLXDDLLEA 9

RESULT 2
US-10-623-176-10
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-2

Query Match 94.7%; Score 36; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.5e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|||||

Db 1 VLXDDLLEA 9

RESULT 3
US-10-623-176-10
; Sequence 10, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-10

Query Match 94.7%; Score 36; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.5e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|||||

Db 1 VLXDDLLEA 9

RESULT 4
US-10-791-217-1
; Sequence 1, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elsa A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/10/791,217
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: obtained from histocompatibility antigen
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is HISTIDINE OR ARGININE RESIDUE
US-10-791-217-1

Query Match 94.7%; Score 36; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|||||

Db 1 VLXDDLLEA 9

RESULT 5
US-10-791-217-2
; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulimy, Elsa A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/10/791,217
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23

NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2

Query Match 94.7%; Score 36; DB 17; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.5e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
DB 1 VLHDDLLEA 9

RESULT 6
US-10-791-217-5
Sequence 5, Application US/10791217
Publication No. US20040191268A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa A.J.M.
APPLICANT: Hunt, Donald F.
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/10/791,217
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: obtained from KIAA0223 partial complementary DNA
US-10-791-217-5

Query Match 94.7%; Score 36; DB 17; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.5e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
DB 1 VLHDDLLEA 9

RESULT 7
US-10-623-176-24
Sequence 24, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa A.J.M.
APPLICANT: Hunt, Donald F.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165

PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
wherein X can be H or R
NAME/KEY: SITE
LOCATION: (1)..(10)
US-10-623-176-24

Query Match 94.7%; Score 36; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
DB 1 VLHDDLLEA 9

RESULT 8
US-10-623-176-43
Sequence 43, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa A.J.M.
APPLICANT: Hunt, Donald F.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 43
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
NAME/KEY: SITE
LOCATION: (1)..(10)
US-10-623-176-43

Query Match 94.7%; Score 36; DB 15; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
DB 1 VLHDDLLEA 9

RESULT 9
US-10-623-176-44
Sequence 44, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulmy, Elsa A.J.M.
APPLICANT: Hunt, Donald F.

```
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
NAME/KEY: SITE
LOCATION: (1)..(10)
US-10-623-176-44
```

```
Query Match          94.7%; Score 36; DB 15; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 VLXDDLEA 9
        |||||||
Db      1 VLRDDLEA 9
```

```
RESULT 10
US-10-623-176-65
Sequence 65, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulimy, Els A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 65
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
NAME/KEY: SITE
LOCATION: (1)..(12)
US-10-623-176-65
```

```
Query Match          94.7%; Score 36; DB 15; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 VLXDDLEA 9
```

```
Db      2 VLRDDLEA 10
        |||||||
```

```
RESULT 11
US-10-623-176-74
Sequence 74, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulimy, Els A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 74
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: KIAA0223
OTHER INFORMATION: sequence derived from a presumed HA-1 negative
NAME/KEY: SITE
LOCATION: (1)..(13)
US-10-623-176-74
```

```
Query Match          94.7%; Score 36; DB 15; Length 13;
Best Local Similarity 88.9%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 VLXDDLEA 9
        |||||||
Db      3 VLRDDLEA 11
```

```
RESULT 12
US-10-623-176-76
Sequence 76, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulimy, Els A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 76
LENGTH: 13
TYPE: PRT
```


ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: KIAA0223
OTHER INFORMATION: sequence derived from a presumed HA-1 Homozygous
FEATURE:
OTHER INFORMATION: positive individual
NAME/KEY: SITE
LOCATION: (1)..(13)
US-10-623-176-76

Query Match 94.7%; Score 36; DB 15; Length 13;
Best Local Similarity 88.9%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||
Db 3 VLHDDLLEA 11

RESULT 13
US-10-791-217-14
Sequence 14, Application US/10791217
Publication No. US20040191268A1
GENERAL INFORMATION:
APPLICANT: Goulimy, Elia A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/10/791,217
PRIOR FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: obtained from HA-1/- phenotype
US-10-791-217-14

Query Match 94.7%; Score 36; DB 17; Length 13;
Best Local Similarity 88.9%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||
Db 3 VLHDDLLEA 11

RESULT 14
US-10-791-217-16
Sequence 16, Application US/10791217
Publication No. US20040191268A1
GENERAL INFORMATION:
APPLICANT: Goulimy, Elia A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: The HA-1 Antigen
FILE REFERENCE: 2183-4285US
CURRENT APPLICATION NUMBER: US/10/791,217
PRIOR FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16

LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: obtained from HA-1/+ phenotype
US-10-791-217-16

Query Match 94.7%; Score 36; DB 17; Length 13;
Best Local Similarity 88.9%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||
Db 3 VLHDDLLEA 11

RESULT 15
US-10-623-176-33
Sequence 33, Application US/10623176
Publication No. US20040092446A1
GENERAL INFORMATION:
APPLICANT: Goulimy, Elia A.J.M.
APPLICANT: Hunt, Donald F.
APPLICANT: Engelhard, Victor H.
TITLE OF INVENTION: HA-1 epitopes and uses thereof
FILE REFERENCE: 2183-6047US
CURRENT APPLICATION NUMBER: US/10/623,176
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/489,760
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: EP 97202303.0
PRIOR FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: PCT/NL98/00424
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: JP 2000-504165
PRIOR FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HA-1
OTHER INFORMATION: polymorphic region wherein X can be H or R
NAME/KEY: SITE
LOCATION: (1)..(17)
US-10-623-176-33

Query Match 94.7%; Score 36; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||
Db 7 VLHDDLLEA 15

Search completed: December 29, 2004, 23:24:41
Job time : 147 secs

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OM protein - protein search, using sw model

Run on: December 29, 2004, 22:58:45 ; Search time 40 Seconds
(without alignments)
21.649 Million cell updates/sec

Title: US-10-791-217A-1

Perfect score: 38

Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	94.7	1165	2	DS9433
2	34	89.5	616	2	C69226
3	33	86.8	174	2	C89075
4	33	86.8	499	2	G85075
5	33	86.8	499	2	G85075
6	32	84.2	112	2	G72083
7	32	84.2	797	2	T50072
8	31	81.6	276	2	AD1291
9	31	81.6	276	2	AD1291
10	31	81.6	276	2	AB1663
11	31	81.6	289	2	C81175
12	31	81.6	397	2	DA1930
13	31	81.6	497	2	A28180
14	31	81.6	750	2	G87793
15	31	81.6	1042	2	B83794
16	31	81.6	72	2	T13647
17	30	78.9	302	2	T26975
18	30	78.9	361	2	AB3246
19	30	78.9	623	2	EA8014
20	30	78.9	683	2	E75221
21	30	78.9	822	2	D82674
22	30	78.9	962	2	D82674
23	30	78.9	962	2	D82674
24	30	78.9	1999	2	AB2018
25	29	76.3	4976	2	T14165
26	29	76.3	101	2	E97582
27	29	76.3	101	2	E97582
28	29	76.3	119	2	AE2803
29	29	76.3	119	2	T35859
29	29	76.3	137	1	Q3ECEA

30	29	76.3	137	2	AI0575	conserved hypotet
31	29	76.3	137	2	D90708	hypothetical prote
32	29	76.3	137	2	H85558	hypothetical prote
33	29	76.3	154	1	R5H830	ribosomal protein
34	29	76.3	156	2	T20267	hypothetical prote
35	29	76.3	178	2	D72293	hypothetical prote
36	29	76.3	192	2	AI2271	transcription regu
37	29	76.3	207	2	G83538	probable oxidoredu
38	29	76.3	231	2	B65140	hypothetical prote
39	29	76.3	231	2	H91164	hypothetical prote
40	29	76.3	231	2	H86010	hypothetical prote
41	29	76.3	244	2	D86725	hypothetical prote
42	29	76.3	251	2	S45438	cytochrome-c oxida
43	29	76.3	277	2	D69158	sensory transducti
44	29	76.3	292	2	S72323	ubiquinol-cytochro
45	29	76.3	322	2	S44847	K0617.7 protein -

ALIGNMENTS

RESULT 1
DS9433
C. elegans protein Z37093 homolog [imported] - human
C:Species: Homo sapiens (man)
C:Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
C:Accession: DS9433; E59433
R:Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayashi, Y.; Ohara, O.; Tanaka, A.
DNA Res. 3, 321-329, 1996
A>Title: Prediction of the coding sequences of unidentified human genes. VI. The coding
A:Reference number: DS9433; MUID:97191544; PMID:9039502
A:Accession: DS9433
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1165 <NMG>
A:Cross-references: UNIPROT:Q92619; GB:BA13212; PID:g1504026; PIDN:BA13212.1
R:Ohara, O.; Nagase, T.; Kikuno, R.; Nomura, N.
Submitted to Genbank, August 1996
A:Reference number: E59433
A:Accession: E59433
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1165 <STO2>
A:Cross-references: GB:BA13212; PID:g1504026; PIDN:BA13212.1

Query Match
Best Local Similarity 94.7%; Score 36; DB 2; Length 1165;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
DB 166 VLXDDLLEA 174

RESULT 2
C69226
Type I restriction modification enzyme, subunit M - Methanobacterium thermoautotrophicum
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
A:Accession: C69226
R:Smith, D.R.; Doncette-Stamm, L.A.; Delongchery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadefora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
K.; S.; Church, G.M.; Daniels, C.J.; Mo, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A>Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: C69226
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-616 <MT1>
A:Cross-references: UNIPROT:O27025; GB:AE000868; GB:AE000666; NID:g2622025; PIDN:AA8544
A:Experimental source: strain Delta H

C:Genetics:
A:Gene: MTH942
A:Start codon: GTG
C:Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 89.5%; Score 34; DB 2; Length 616;
Best Local Similarity 77.8%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||:||||
DB 465 VLIEDLLER 473

RESULT 3
C89075
protein K04A8.9 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: C89075
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: C89075
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-174 <STO>
A:Cross-references: UNIPROT:Q94256; GB:chr_V; PIDN:AAc48055.1; PID:g1658358; GSPDB:GN000
C:Genetics:
A:Gene: K04A8.9
A:Map position: 5

Query Match 86.8%; Score 33; DB 2; Length 174;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||:||||
DB 129 VLKDDLLEA 137

RESULT 4
G86538
leucyl aminopeptidase A [imported] - Chlamydia pneumoniae (strain U138)
C:Species: Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86538
R:Shitai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae U138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: G86538
A:Status: preliminary
A:Residues: 1-499 <STO>
A:Molecule type: DNA
A:Cross-references: UNIPROT:Q928F8; GB:BA000008; NID:g8978757; PIDN:BAa98593.1; GSPDB:GN
C:Genetics:
A:Gene: pepA
C:Superfamily: Cytosol aminopeptidase

Query Match 86.8%; Score 33; DB 2; Length 499;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||:||||
DB 395 VLAEDDLLEA 403

RESULT 5
G72083
leucine aminopeptidase CP0370 [imported] - Chlamydia pneumoniae (strains CML029 and
N:Alternate names: leucyl aminopeptidase A
C:Species: Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: G72083; F81583
R:Kauman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: G72083
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-499 <ARN>
A:Cross-references: UNIPROT:Q928F8; GB:AE001623; GB:AE001363; NID:g4376662; PIDN:AAI1852

A:Experimental source: strain CML029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MOpn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: F81583
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-499 <REA>
A:Cross-references: GB:AE002199; GB:AE002161; NID:g7189293; PIDN:AAf38219.1; PID:g718929

A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: pepA; CP0370
C:Superfamily: Cytosol aminopeptidase

Query Match 86.8%; Score 33; DB 2; Length 499;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
|||:||||
DB 395 VLAEDDLLEA 403

RESULT 6
S33180
nitrogen regulatory protein P-II - Rhodospirillum rubrum
C:Species: Rhodospirillum rubrum
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S33180
R:Zinchenko, V.V.; Churru, U.N.; Shestopalov, V.I.; Shestakov, S.V.
submitted to the EMBL Data Library, April 1993
A:Description: Nucleotide sequence and characterization of glnBA operons of the purple p
A:Reference number: S33180
A:Accession: S33180
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-112 <ZIN>
A:Cross-references: UNIPROT:P43519; EMBL:X71659; NID:g297112; PIDN:CAa50650.1; PID:g8097
A:Experimental source: strain 2R
C:Genetics:
A:Gene: glnB
A:Start codon: GTG
C:Function:
A:Description: important for the control of glutamine synthase; in nitrogen-limiting con
to form P-II-UWP; P-II-UWP allows the deadenylation of glutamine synthetase, thus activa
GS
A:Note: P-II indirectly controls the transcription of the GS gene (glnA) by preventing N

Query Match 84.2%; Score 32; DB 2; Length 112;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|||:|
64 VLADDMVER 72

RESULT 7

hypotheetical protein SPAC1486.03c [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
R:McDougal, R.C.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
submitted to the EMBL Data Library, December 1999
A:Reference number: 225034
A:Accession: T50072
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-797 <MCD>
A:Cross-references: UNIPROT:Q9UTK6; EMBL:AL133357; PIDN:CAB62413.1; GSPDB:GN00066; SPDB:
C:Genetics:
A:Gene: SPDB:SPAC1486.03c
A:Map position: 1

Query Match 84.2%; Score 32; DB 2; Length 797;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|||:|
81 VTADDLLEA 89

RESULT 8

sugar ABC transporter, permease protein homolog lmo1732 [imported] - Listeria monocytogenes
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AD1291
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshl, H.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; Ma
ok, C.; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1291
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <GLA>
A:Cross-references: UNIPROT:Q8Y6F5; GB:NC_003210; PIDN:CAC99810.1; PID:G16411186; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1732
C:Superfamily: maltose transport protein malG

Query Match 81.6%; Score 31; DB 2; Length 276;
Best Local Similarity 75.0%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LKDDLLEA 9
:|||||
165 ISDDLLEA 172

RESULT 9

sugar ABC transporter, permease protein homolog lln1843 [imported] - Listeria innocua (S
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB1663

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshl, H.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; Ma
ok, C.; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1663
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <GLA>
A:Cross-references: UNIPROT:Q92AS6; GB:AL592022; PIDN:CAC97074.1; PID:G16414345; GSPDB:
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lln1843
C:Superfamily: maltose transport protein malG

Query Match 81.6%; Score 31; DB 2; Length 276;
Best Local Similarity 75.0%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LKDDLLEA 9
:|||||
165 ISDDLLEA 172

RESULT 10

UTP-glucose-1-phosphate uridylyltransferase NMB0638 [imported] - Neisseria meningitidis
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: CB1175
R:Retelijn, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Bisen, J.P.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.,
.; H.; Qin, H.; Vamthavan, V.; Gill, J.; Scarlato, V.; Maignan, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Frazer, C.M.; Moxon, E.R.; Rappoli, R.; V
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755; PMID:10710307
A:Accession: CB1175
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <TEP>
A:Cross-references: UNIPROT:Q9K0G7; GB:AE002419; GB:AE002098; NID:G7225863; PIDN:AAF4106
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0638
C:Superfamily: Escherichia coli UTP-glucose-1-phosphate uridylyltransferase

Query Match 81.6%; Score 31; DB 2; Length 289;
Best Local Similarity 55.6%; Pred. No. 74;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
:|||||
130 TLADDLLEA 138

RESULT 11

probable UTP-glucose-1-phosphate uridylyltransferase NMA0848 [imported] - Neisseria men
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: DB1930
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: AB1775; MUID:20222556; PMID:10761919
A:Accession: DB1930
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-289 <PAR>
A:Cross-references: UNIPROT:Q9JVG6; GB:AL162754; GB:AL157959; NID:G7379424; PIDN:CB8412
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: galV; NMA0848
C:Superfamily: Escherichia coli UTP-glucose-1-phosphate uridylyltransferase

Query Match
Best Local Similarity 81.6%; Score 31; DB 2; Length 289;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
: |||||
DB 130 ILADDLLEA 138

RESULT 12
A28180
carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) large chain - Methanos
N:Alternate names: carbamoyl-phosphate synthetase (glutamine-hydrolyzing), ammonia chain
C:Species: Methanogarcina barkeri
C>Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 09-Jul-2004
C:Accession: A28180
R:Morris, C.J.; Reeve, J.N.
J. Bacteriol. 170, 3125-3130, 1988
A:Title: Conservation of structure in the human gene encoding argininosuccinate synthetase
A:Reference number: A91873; MUID:88257029; PMID:3133361
A:Accession: A28180
A:Molecule type: DNA
A:Residues: 1-397 <MOR>
A:Cross-references: UNIPROT:P13258
C:Genetics:
A:Gene: canB
C:Keywords: arginine biosynthesis; ligase; pyrimidine nucleotide biosynthesis
F:1-308/Domain: diocin carboxylase homology <BCH>

Query Match
Best Local Similarity 81.6%; Score 31; DB 2; Length 397;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
: |||||
DB 67 ILIDDLLEA 75

RESULT 13
G87793
protein C27A12.7 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G87793
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C.elegans/ and www_sanger.ac.uk/Projects/C_elg
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: G87793
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-497 <STO>
A:Cross-references: UNIPROT:O01964; GB:chr_I; PIDN:AAB93644.1; PID:G2105479; GSPDB:GN000
C:Genetics:
A:Gene: C27A12.7
A:Map position: 1

Query Match
Best Local Similarity 81.6%; Score 31; DB 2; Length 497;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
: |||||
DB 55 VLIDDLLEA 63

RESULT 14
B83794
hypothetical protein BH1154 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: B83794
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B83794
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-750 <STO>
A:Cross-references: UNIPROT:Q9K007; GB:AP001511; GB:BA000004; NID:G10173727; PIDN:BA8048
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1154

Query Match
Best Local Similarity 81.6%; Score 31; DB 2; Length 750;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
: |||||
DB 581 ILIDDLLEA 589

RESULT 15
T13647
hypothetical protein 95B7.8 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13647
R:Perraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
Submitted to the EMBL Data Library, April 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17694
A:Accession: T13647
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1042 <FER>
A:Introns: 94/3; 833/3; 937/3
A:Cross-references: UNIPROT:O76911; EMBL:AL021728; PIDN:CAA16820.1
C:Genetics:
A:Cross-references: FlyBase:FBgn0000376
A:Introns: 94/3; 833/3; 937/3
A>Note: EG:95B7.8
C:Superfamily: fruit fly hypothetical protein EG_95B7.8

Query Match
Best Local Similarity 81.6%; Score 31; DB 2; Length 1042;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
: |||||
DB 595 VLFDLLEA 603

Search completed: December 29, 2004, 23:13:34
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 22:57:40 ; Search time 188 Seconds.

(without alignments)
27.545 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 38
Sequence: 1 VLXDDLLEA 9

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	94.7	668	06LZ81	Q6LZ81 mechanococ
2	36	94.7	668	CAF30304	Q6LZ81 mechanococ
3	36	94.7	1131	081YN3	Q81YN3 homo sapien
4	36	94.7	1136	06P189	Q6P189 homo sapien
5	36	94.7	1136	08HX84	Q8HX84 homo sapien
6	36	94.7	1136	AAH65223	AAH65223 homo sapi
7	36	94.7	1165	092619	Q92619 homo sapien
8	35	92.1	585	08EJ89	Q8EJ89 shewanella
9	34	89.5	146	074B30	Q74B30 geobacter s
10	34	89.5	146	AAH35828	AAH35828 geobacter
11	34	89.5	376	Q8WV81	Q8WV81 ixodes scap
12	34	89.5	616	027025	Q27025 mechanobact
13	33	86.8	174	094256	Q94256 caenorhabdi
14	33	86.8	185	082P65	Q82P65 streptomyce
15	33	86.8	291	081SV5	Q81SV5 bacillus an
16	33	86.8	291	AAH35306	AAH35306 bacillus
17	33	86.8	292	Q6HL66	Q6HL66 bacillus th
18	33	86.8	292	061163	Q61163 bacillus an
19	33	86.8	292	081FT0	Q81FT0 bacillus ce
20	33	86.8	499	1 AMPA_CHLPN	Q92858 chlamydia p
21	32	84.2	112	1 GMB_RHOSH	P43519 rhodobacter
22	32	84.2	112	031158	Q31158 rhodobacter
23	32	84.2	436	Q8EP44	Q8EP44 oceanobacti
24	32	84.2	616	Q50407	Q50407 mycobacteri
25	32	84.2	797	Q9UTK6	Q9UTK6 schizosacch
26	32	84.2	800	08FTX1	Q8FTX1 corynobacte
27	32	84.2	894	09FMC7	Q9FMC7 oryza sativ
28	32	84.2	920	07RYV8	Q7RYV8 neurospora
29	32	84.2	1155	0852F5	Q852F5 oryza sativ
30	32	84.2	2041	07S374	Q7S374 neurospora
31	32	84.2	4150	09KIV4	Q9KIV4 streptomyce

32	31	81.6	169	2	Q73B06	Q73B06 bacillus ce
33	31	81.6	169	2	AA540543	AA540543 bacillus
34	31	81.6	226	2	Q7OMX4	Q7OMX4 anophelis g
35	31	81.6	263	2	Q98L75	Q98L75 rhizobium l
36	31	81.6	276	2	Q92A86	Q92A86 listeria in
37	31	81.6	276	2	Q8Y6F5	Q8Y6F5 listeria mo
38	31	81.6	276	2	Q71Y76	Q71Y76 listeria mo
39	31	81.6	276	2	AA704528	AA704528 listeria
40	31	81.6	289	2	Q9JVG6	Q9JVG6 neisseria m
41	31	81.6	289	2	Q9K0G7	Q9K0G7 neisseria m
42	31	81.6	293	2	Q8H305	Q8H305 oryza sativ
43	31	81.6	299	2	Q83VQ1	Q83VQ1 methylolact
44	31	81.6	306	1	ISH1_RHOPA	Q6N3G0 rhodospir
45	31	81.6	306	2	CAE29175	CAE29175 rhodospir

ALIGNMENTS

RESULT 1						
06LZ81	PRELIMINARY;	PRT;	668	AA.		
AC	06LZ81;					
DT	05-JUL-2004 (TREMBLrel. 27, Created)					
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)					
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)					
DE	MCM family related protein.					
GN	OrderedLocustNames=MMP0748;					
OS	Methanococcus maripaludis.					
OC	Archaea; Euryarchaeota; Methanococci; Methanococcales;					
OC	Methanococcaceae; Methanococcus.					
OX	NCBI_TaxID=39152;					
RP	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=S2 / LI;					
RA	Hendrickson E.L., Kaul R., Zhou Y., Boyse D., Chapman P., Chung J.,					
RA	Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,					
RA	Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,					
RA	Moore B., Porat I., Overbeek R., Palmeri A., Rouse G.,					
RA	Saenphimmachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,					
RA	Leigh J.A.;					
RT	"Complete genome sequence of the mesophilic hydrogenotrophic					
RT	methanogen Methanococcus maripaludis."					
RL	Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.					
DR	EMBL: BX957221; CAF30304.1; -					
DR	InterPro: IPR002048; EF-hand.					
DR	InterPro: IPR001208; MCM.					
DR	Pfam: PF00493; MCM; 1.					
DR	PRINTS: PR01657; MCMFAMILY.					
DR	PRODOM: PD001041; MCM; 1.					
DR	SMART: SM00350; MCM; 1.					
DR	PROSITE: PS00018; EF_HAND; UNKNOWN_1.					
DR	PROSITE: PS50051; MCM_2; 1.					
KW	Complete proteome.					
SQ	SEQUENCE 668 AA; 75660 MW; 2ADAF3800B1049FA CRC64;					
Query Match						
Best Local Similarity			94.7%	Score 36;	DB 2;	Length 668;
Matches 8;			Conservative	0;	Mismatches 1;	Indels 0;
Gaps 0;						
Qy	1	VLXDDLLEA 9				
Db	628	VLXDDLLEA 636				
RESULT 2						
CAF30304	PRELIMINARY;	PRT;	668	AA.		
ID	CAF30304;					
AC	CAF30304;					
DT	03-MAR-2004 (TREMBLrel. 27, Created)					
DT	03-MAR-2004 (TREMBLrel. 27, Last sequence update)					
DT	04-MAY-2004 (TREMBLrel. 27, Last annotation update)					
DE	MCM family related protein.					

GN MMP0748.
OS Methanococcus maripaludis.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=39152;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=52 / L1;
RA Hendrickson E.L., Kaul R., Zhou Y., Boyce D., Chapman P., Chung J.,
RA Conway de Macario E., Dodsworth J., Gillett W., Graham D.B.,
RA Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
RA Moore B., Port I., Overbeek R., Palmeiri A., Rouse G.,
RA Saenphummachak C., Seell D., Whitman W.B., Larimer F.W., Olson M.V.,
RA Leigh J.A.;
RT "Complete genome sequence of the mesophilic hydrogenotrophic
RT Methanogen Methanococcus maripaludis";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BX957221; CAF30304.1; --
SQ SEQUENCE 668 AA; 75660 MW; 2ADAF380B1049F4 CRC64;

Query Match 94.7%; Score 36; DB 2; Length 668;
Best Local Similarity 88.9%; Pred. No. 1;le+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
DB 628 VLXDDLLEA 636

RESULT 3
QIDYN3 PRELIMINARY; PRT; 1131 AA.
AC Q8IYN3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to PTP1-associated RhoGAP 1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC035564; AAH35564.1; --
DR HSRP, Q88935; 1F7C.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001060; Cdc15_Fes_CIP4.
DR InterPro; IPR000345; Cyclic_heme_BS.
DR InterPro; IPR002219; DAG_Fe-bind.
DR InterPro; IPR000198; RhoGAP.
DR InterPro; IPR008936; Rho_GAP.
DR Pfam; PF00130; C1_1; 1.
DR Pfam; PF00620; RhoGAP; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00055; FCH; 1.
DR SMART; SM00324; RhoGAP; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00479; DAG_Fe_BIND_DOM_1; UNKNOWN_1.
DR PROSITE; PS50081; DAG_Fe_BIND_DOM_2; 1.
DR PROSITE; PS50238; RHO_GAP; 1.
FT NON TER 1
SQ SEQUENCE 1131 AA; 124081 MW; A606B1AA52014925 CRC64;

Query Match 94.7%; Score 36; DB 2; Length 1131;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
DB 132 VLXDDLLEA 140

RESULT 4
Q6P189 PRELIMINARY; PRT; 1136 AA.
AC Q6P189;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Minor histocompatibility antigen HA-1.
GN Name=HA-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinchi P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC065223; AAH65223.1; --
DR InterPro; IPR001060; Cdc15_Fes_CIP4.
DR InterPro; IPR000345; Cyclic_heme_BS.
DR InterPro; IPR002219; DAG_Fe-bind.
DR InterPro; IPR000198; RhoGAP.
DR InterPro; IPR008936; Rho_GAP.
DR Pfam; PF00130; C1_1; 1.
DR Pfam; PF00620; RhoGAP; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00055; FCH; 1.
DR SMART; SM00324; RhoGAP; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00479; DAG_Fe_BIND_DOM_1; UNKNOWN_1.
DR PROSITE; PS50081; DAG_Fe_BIND_DOM_2; 1.
DR PROSITE; PS50238; RHO_GAP; 1.
SQ SEQUENCE 1136 AA; 124550 MW; 14B7073296102DD5 CRC64;

Query Match 94.7%; Score 36; DB 2; Length 1136;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDDLLEA 9
DB 137 VLXDDLLEA 145

RESULT 5
Q8HX84 PRELIMINARY; PRT; 1136 AA.

AC Q8HX84;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Minor histocompatibility antigen HA-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20549028; PubMed=11095984;
 RA Kaminski W.E., Plehler A., Schmitz G.;
 RT "Genomic organization of the human cholesterol-responsive ABC
 RT transporter ABCA7: tandem linkage with the minor histocompatibility
 RT antigen HA-1 gene.";
 RL Biochem. Biophys. Res. Commun. 278: 782-789 (2000).
 DR EMBL; AF308045; AAN04658.1; JOINED.
 DR EMBL; AF308046; AAN04658.1; JOINED.
 DR EMBL; AF308047; AAN04658.1; JOINED.
 DR EMBL; AF308048; AAN04658.1; JOINED.
 DR EMBL; AF308049; AAN04658.1; JOINED.
 DR EMBL; AF308050; AAN04658.1; JOINED.
 DR EMBL; AF308051; AAN04658.1; JOINED.
 DR EMBL; AF308052; AAN04658.1; JOINED.
 DR EMBL; AF308053; AAN04658.1; JOINED.
 DR EMBL; AF308054; AAN04658.1; JOINED.
 DR EMBL; AF308055; AAN04658.1; JOINED.
 DR EMBL; AF308056; AAN04658.1; JOINED.
 DR EMBL; AF308057; AAN04658.1; JOINED.
 DR EMBL; AF308058; AAN04658.1; JOINED.
 DR EMBL; AF308059; AAN04658.1; JOINED.
 DR EMBL; AF308060; AAN04658.1; JOINED.
 DR EMBL; AF308061; AAN04658.1; JOINED.
 DR EMBL; AF308062; AAN04658.1; JOINED.
 DR EMBL; AF308063; AAN04658.1; JOINED.
 DR EMBL; AF308064; AAN04658.1; JOINED.
 DR EMBL; AF308065; AAN04658.1; JOINED.
 DR EMBL; AF311102; AAN04658.1; JOINED.
 DR HSSP; Q98935; 1F7C.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR InterPro; IPR001060; Cdc15_Fes_CIP4.
 DR InterPro; IPR000345; CycC_Fes_BS.
 DR InterPro; IPR002219; DAG_Fe-bind.
 DR InterPro; IPR000198; RhoGAP.
 DR InterPro; IPR008936; Rho_GAP.
 DR Pfam; PF00130; C1_1; 1.
 DR Pfam; PF00620; RhoGAP; 1.
 DR SMART; SM00109; C1; 1.
 DR SMART; SM00055; FCH; 1.
 DR SMART; SM00324; RhoGAP; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS50238; RHO_GAP; 1.
 SQ SEQUENCE 1136 AA; 124613 MW; 9536787B3B1E1D CRC64;

Query Match 94.7%; Score 36; DB 2; Length 1136;
 Best Local Similarity 88.9%; Pred. No. 2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
 Db 137 VLXDDLLEA 145

RESULT 6
 AAH65223 PRELIMINARY; PRT; 1136 AA.
 AC AAH65223;
 DT 02-MAR-2004 (TRENBLrel. 27, Created)
 DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
 DE Minor histocompatibility antigen HA-1.
 GN HA-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JAN-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC065223; AAH65223.1;
 SQ SEQUENCE 1136 AA; 124550 MW; 14B7073296102DD5 CRC64;

Query Match 94.7%; Score 36; DB 2; Length 1136;
 Best Local Similarity 88.9%; Pred. No. 2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
 Db 137 VLXDDLLEA 145

RESULT 7
 Q92619 PRELIMINARY; PRT; 1165 AA.
 AC Q92619;
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE KIA0223 protein (Fragment).
 GN Name=KIA0223;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=bone marrow;
 RX MEDLINE=97191544; PubMed=9039502;
 RA Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayashi Y., Ohara O.,
 RA Tanaka A., Kotani H., Miyajima N., Nomura N.;
 RT "Prediction of the coding sequences of unidentified human genes. VI.
 RT The coding sequences of 80 new genes (KIA0201-KIA0280) deduced by
 RT analysis of cDNA clones from cell line KG-1 and brain.";
 RL DNA Res. 3:321-329 (1996).
 DR EMBL; D86976; BAA13212.1;
 DR PIR; D59433; D59433.

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DR GO:0007242; P:intracellular signaling cascade; IEA.
DR InterPro: IPR001060; Cdc15_Fes_CIP4.
DR InterPro: IPR000345; CycC_heme_BS.
DR InterPro: IPR002219; DAG_Pe-bind.
DR InterPro: IPR000198; RhoGAP.
DR InterPro: IPR008936; Rho_GAP.
DR Pfam: PF00130; C1_1; 1.
DR Pfam: PF00620; RhoGAP; 1.
DR SMART: SM00109; C1; 1.
DR SMART: SM00055; FCH; 1.
DR SMART: SM00324; RhoGAP; 1.
DR PROSITE: PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_1.
DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS50238; RHO GAP; 1.
DR NON TER
FT SEQUENCE 1165 AA; 127344 MW; 92EF768CAF58C9 CRC64;

Query Match
Best Local Similarity 94.7%; Score 36; DB 2; Length 1165;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
Db 166 VLXDDLLEA 174

RESULT 8
OEBJS9 PRELIMINARY; PRT; 585 AA.
ID OEBJS9
AC OEBJS9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 23, Last annotation update)
DE Type I restriction-modification system, M subunit.
GN Name-hsGM-1; OrderedLocustNames=SO0383;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gallos B.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beaman M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA Lee K., Berry K.J., Lee C., Muehlner J., Khouli H.M., Gill J.,
RA Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123 (2002).
DR EMBL; AE015486; AAN53466.1; -.
DR TIGR; S00383; -.
DR GO:0003677; F:DNA binding; IEA.
DR GO:0008170; F:N-methyltransferase activity; IEA.
DR GO:0009007; F:site-specific DNA-methyltransferase (adenin. . .); IEA.
DR GO:0006306; P:DNA methylation; IEA.
DR GO:0006304; P:DNA modification; IEA.
DR InterPro: IPR004546; HsdM.
DR InterPro: IPR003665; Methylase M.
DR InterPro: IPR002296; N12N6_mtfase.
DR InterPro: IPR003356; N6_DNA_mtfase.
DR InterPro: IPR002052; N6_Mtfase.
DR Pfam; PF02506; Methylase_M; 1.
DR Pfam; PF02384; N6_Mtfase; 1.
DR PRINTS; PR00507; N12N6MTFRASE.
DR TIGRPFAM; TIGR00497; hsdM; 1.
DR PROSITE; PS00092; N6_MTFASE; UNKNOWN_1.

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KW Complete proteome.
SQ SEQUENCE 585 AA; 66321 MW; 349D45BF52C98D0C CRC64;

Query Match
Best Local Similarity 92.1%; Score 35; DB 2; Length 585;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
Db 335 ILMDLLEA 343

RESULT 9
O74B30 PRELIMINARY; PRT; 146 AA.
ID O74B30
AC O74B30;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DB Hypothetical protein.
GN ORFNames=GSU2455;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beaman M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouli H.M., Feldblyum T.V., Uterback T.R.,
RA Van Aken S.E., Loyley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments."
RL Science 302:1967-1969 (2003).
DR EMBL; AE017180; AAR35828.1; -.
DR TIGR; GSU2455; -.
DR InterPro: IPR005361; UPR0158.
DR ProDom; PD191405; UPR0158; 1.
KW Hypothetical protein.
SQ SEQUENCE 146 AA; 17581 MW; 30B46BBE69DE5255 CRC64;

Query Match
Best Local Similarity 89.5%; Score 34; DB 2; Length 146;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
Db 9 ILMDLLEA 17

RESULT 10
AAR35828 PRELIMINARY; PRT; 146 AA.
ID AAR35828
AC AAR35828;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN GSU2455.
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,

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RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gillin M.L., Kolman J.F., Sullivan S.A., Haft D.H., Selengut J.,
 RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J.E., Koutz H.M., Feldblyum T.V., Uterback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.,
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 environments";
 RL Science 302:1967-1969 (2003).
 DR EMBL: AE017215; AAR35828.1; --
 KW TIGR; GSU2455; --
 SQ SEQUENCE 146 AA; 17581 MW; 30846BEE69DE5255 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 146;
 Best Local Similarity 77.8%; Pred. No. 60;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VLXDDLLEA 9
 Db 9 ILMDLLEA 17

RESULT 11
 Q8WB1 PRELIMINARY; PRT; 376 AA.
 ID Q8WB1;
 AC Q8WB1;
 DT 01-OCT-2002 (TRENBLrel. 22, Last created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DB Putative serine protease with signal anchor.
 OS Ixodes acapulensis (black-legged tick) (Deer tick).
 CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 CC Parasitiformes; Ixodida; Ixodidae; Ixodes.
 OX NCBI_Taxid=6945;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rhode Island; TISSUE=Salivary gland;
 RA Valenzuela J.G., Francischetti I.M., Pham V.M., Garfield M.,
 RA Mather T.N., Ribeiro J.M.C.;
 RL Submitted (FEB-2002) to the EMBL/Genbank/DDJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family 51.
 DR EMBL: AF483729; AAM93651.1; --
 DR GO; GO:0004263; F:cytochrome-c oxidase activity; IEA.
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006118; F:electron transport; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR003204; Cyt_C_Ox5A.
 DR InterPro: IPR001545; Gly_hormoneB.
 DR InterPro: IPR001354; Peptidase_S1.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR InterPro: IPR009003; Pept_Ser_Cys.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SMO0020; Tryp_SPC; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PSS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 376 AA; 41434 MW; 64F403CAD505CD33 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 376;
 Best Local Similarity 77.8%; Pred. No. 1.6e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VLXDDLLEA 9
 Db 245 VLMDLLEA 253

RESULT 12

O27025 PRELIMINARY; PRT; 616 AA.
 ID O27025;
 AC O27025;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DB Type I restriction modification enzyme, subunit M.
 GN OrderedLocustNames=MT1942;
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_Taxid=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jivani N., Caruso A., Bush D., Sater H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 deltaH: functional analysis and comparative genomics";
 RL J. Bacteriol. 179:7135-7155 (1997).
 DR EMBL: AE000868; AAB85440.1; --
 DR PIR: C69226; C69226.

DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
 DR GO; GO:0009007; F:site-specific DNA-methyltransferase (adenin. .); IEA.
 DR GO; GO:0006306; P:DNA methylation; IEA.
 DR GO; GO:0006304; P:DNA modification; IEA.
 DR InterPro: IPR003655; Methylase_M.
 DR InterPro: IPR002296; N12N6_mtfase.
 DR InterPro: IPR003356; N6_DNA_Mcase.
 DR InterPro: IPR002052; N6_DNA_Mcase.
 DR InterPro: IPR009058; Wing_hlx_DNA_bnd.
 DR Pfam: PF02506; Methylase_M; 1.
 DR Pfam: PF02384; N6_Mcase; 1.
 DR PRINTS; PR00507; N12N6MTFRASE.
 DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 616 AA; 71715 MW; 06D4F1076A5D5BAD CRC64;

Query Match 89.5%; Score 34; DB 2; Length 616;
 Best Local Similarity 77.8%; Pred. No. 2.7e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VLXDDLLEA 9
 Db 465 VLMDLLEA 473

RESULT 13
 O94256 PRELIMINARY; PRT; 174 AA.
 ID O94256;
 AC O94256;
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DB Saposin-like protein family protein 19.
 GN Name=spp-19;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;

"Genome sequence of the nematode C. elegans: a platform for

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RT Investigating biology. The C. elegans Sequencing Consortium." ;
RL Science 283:2012-2018(1998) .
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2.
RA Geisel C., Bradshaw H.,
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2.
RA Waterston R.,
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2.
RA Wilson R.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U64849; AAC48055.1; -.
DR PIR; C89075; C89075.
DR WormPep; K04A8.9; CE11716.
DR InterPro; IPR008139; SaposinB.
DR InterPro; IPR011001; Saposin_Like.
DR SMART; SM00741; SapB; 1.
SQ SEQUENCE 174 AA; 19210 MW; A6303CF6383BBE09 CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 2; Length 174;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLXDLLEA 9
DB 129 VLXDDLDA 137

RESULT 14
ID Q82P65 PRELIMINARY; PRT; 185 AA.
AC Q82P65;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative TetR-family transcriptional regulator.
GN OrderedLocustNames=SAV1068;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites." ;
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RL "Complete genome sequence and comparative analysis of the industrial
RL microorganism Streptomyces avermitilis." ;
RL Nat. Biotechnol. 21:526-531(2003) .
CC -1- SIMILARITY: Contains 1 HTH TetR-type DNA-binding domain.
DR EMBL; AP005025; BAC68778.1; -.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
DR InterPro; IPR001241; DNA_topoisom1.
DR InterPro; IPR009057; Homeodomain_Like.
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DR InterPro; IPR001647; HTH_TetR.
DR Pfam; PF00440; HTH_N; 1.
DR PRINTS; PR00455; HTH_TETR.
DR PROSITE; PS00177; TOPOTISOMERASE_II; UNKNOWN 1.
KW Complete proteome; DNA-binding; Transcription regulation.
SQ SEQUENCE 185 AA; 19715 MW; 36580407CCD54C30 CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 2; Length 185;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LXDILLEA 9
DB 171 LXDILLEA 178

RESULT 15
ID Q81SY5 PRELIMINARY; PRT; 291 AA.
AC Q81SY5; Q6KJB0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Transcriptional regulator, Meir family.
GN OrderedLocustNames=BA1509; ORFNames=GBAA1509;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / Isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillye L.W., Paulsen I.T.,
RA Nelson K.E., Tetteijn H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapfel E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beaman M.J., Dodson R.O., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin H.M., Radune D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Kouri H.M., Radune D.F.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Platt R.D., Wolf A.M., Mackinnon K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria." ;
RL Nature 423:81-86(2003) .
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / Isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics." ;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017028; AAP25446.1; -.
DR EMBL; AB017334; AAT35306.1; -.
DR TIGR; BA1509; -.
DR GO; GO:0005623; C:intracellular; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
DR InterPro; IPR011007; B12_binding.
DR InterPro; IPR000551; HTH_Meir.
DR Pfam; PF00376; Meir; 1.
DR SMART; SM00422; HTH_Meir; 1.
DR PROSITE; PS50937; HTH_Meir_2; 1.
KW Complete proteome; DNA-binding.
SQ SEQUENCE 291 AA; 33164 MW; D96019E1884B142D CRC64;

Query Match
Best Local Similarity 86.8%; Score 33; DB 2; Length 291;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 VLXDDLEA 9
          |||||:|
Db      94 VLVDLLQA 102
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Job time : 192 secs

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